

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number:99177

TO: Rebecca Prouty

Location: cm-1/10a13/10d01

Art Unit: 1652

Friday, August 01, 2003

Case Serial Number: 10/089986

From: Toby Port

Location: Biotech-Chem Library

CM1-6A04

Phone: 308-3534

toby.port@uspto.gov

Search Notes

Dear Examiner Prouty,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port

BEST AVAILABLE COPY



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Sequence 551, Appli Sequence 259845. Sequence 4627, Appli Sequence 24, Appli Sequence 213361. Sequence 206, Appli Sequence 211, Appli Sequence 502, Appli Sequence 6502, Appli Sequence 71236, Appli Sequence 71236, Appli Sequence 71236, Appli Sequence 71236, Appli

Sequence 5, Appli Sequence 1, Appli Sequence 142839, Sequence 3, Appli Sequence 4021, Ap Sequence 37, Appl Sequence 2805, Appli Sequence 2805, Appli

Searched:

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34, Appl 76212, i

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298 GTCGAACCACACATTAAAATAACAGACTCAATGATGGCAAAGCAGATCCCCTTGGCAAT 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1648, Application US/09880107
Fatent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: HORNAY
APPLICANT: HORNAY
APPLICANT: HORNAY
APPLICANT: HORNAY
APPLICANT: GENERAL
APPLICANT: Scherf, Uwe
TILLE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT APPLICATION NUMBER: US 60/211,379
FRIOR FILING DATE: 2000-06-14
FRIOR FILING DATE: 2000-10-02
SOFTWARE FREE PAREATH Ver. 2.1
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US-09-880-107-1648
2 US-09-995-898A-28

US-08-710-027-632-233098

US-08-710-986A-551

US-09-790-988-1

US-09-938-842A-4627

US-09-938-842A-4627

US-09-887-576-37

US-09-887-576-37

US-10-114-170-206

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US-09-10-27-632-33842

US-09-10-632-71236

US-10-027-632-71236

US-10-027-632-71236

US-09-815-242-6598

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Best Local Similarity 48.6%; Pred. No. 9.1e-11;
Matches 297; Conservative 0; Mismatches 302;
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LENGTH: 1356
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7112.734 Million cell updates/sec
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/cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
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                 version 5.1.6
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US-09-960-352-6109
US-09-918-995-15653
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US-10-239-676-209
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US-10-079-854-292
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Maximum Match 1008
Listing first 45 summaries
                                                                                    nucleic search, using sw model
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                   GenCore Copyright (c) 1993
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Maximum DB seq length: 2000000000
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233 GTTGATAAAACAACCTCATGCTGCTTCGGAGGGAAGGATTACTCTGAAATGTACGTGACC 292
                                                             ATACCGTAAAAATACCAGATCCTCAGGTCACCTCTGTAGCATTTGGCGGTCCGAATTTGG
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APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR APPLICATION NUMBER: US/09/235,076

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FASELSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43.6; DB 12;
Pred. No. 0.035;
0; Mismatches 179;
                                                                                                                                        871 TACAGAGTAACAGGTTTAGGCGTCAAAGG 899
                                                                                                                                                                                                                                                 ; Sequence 15653, Application US/09918995; Publication No. US20030073623A1; GENERAL INFORMATION:
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8.09-960-352-8453
Sequence 8453, Application US/09960352
Patent No. US20020137139A1
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COTHER INFORMATION: n = A,T,C or
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nilarity 48.9%;
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Matches 180; Conserve
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APPLICANT: Tao, Nengbing
APPLICANT: Byatt. John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: NUSCLE AND FAT DEPOSITION
TITLE OF ILL OF THE REFERENCE: 16511.006/37-21(10298)
TITLE OF THE REFERENCE: 16511.006/37-21(10298)
THE REFERENCE: 16511.006/37-21(10298)
THIS OF THE REFERENCE: 15111.006/37-21
THING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGGTCTTTTGAGGCAACCTGAAGCTGGAATTTTCAAGATAAACTGGTCTGGGGGTC 960
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                                                                                     GCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATATTTGATTCGGGGAAA 534
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           AGTTTATATCATTTAGGGGCTGATAAAAGGTAAAAATGCACGAGGAGCAACATAGCTATA 474
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                                                                                                                        550 TCCAATGGTTTGGATTGGTCGCTAGACCACAAATCTTCTATTACATTGACAGCCTGTCC
                                                                                                                                                                AGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTATCCATCAGCAATCAACGGCCA
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                                                 GCCCTGTACTCCCTCTTTCCTGATCACCACGTGAAAAAGTACTTTGACCAGGTGGACATT
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Pred. No. 0.025;
0; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: CLone ID: 26-LIB34-038-Q1-E1-G9
US-09-960-352-6109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6109, Application US/09960352 Patent No. US20020137139A1 GENERAL INFORMATION:
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Best Local Similarity 50.23
Matches 135; Conservative
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961 AAAGGAATTGC 971
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    GATCATGAAACTCAGACCTTATATTTCGTCGACACCGTAGAGAAAACTTTTCATAAATAT 126
                                                                                                                         Sequence 116286, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, David G. TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.1.29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR PELICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR PELICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASESEQ for Windows Version 4.0
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59.4%; Pred. No. 6.
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PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PRILIC DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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                                                                                                                                                                                                                                        US-10-027-632-116285; Sequence 116285, Application US/10027632; GENERAL INFORMATION:
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63; Conserv
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Best Local S
Matches 63
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                                          APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Magapan
APPLICANT: Mathalagan, Magapan
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352.
CURRENT FILING DATE: 2001-09-24
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: .2002-09-24
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Pred. No. 0.65;
0; Mismatches 110; Indels
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; OTHER INFORMATION: Clone ID: 36-LIB34-030-01-E1-A8
US-09-960-352-8453
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Pred. No. 5.2;
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DE 10019058.8
DE 10019173.8
DE 10035529.7
DE 100343826.1
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2000-04-06
2000-04-07
2000-06-30
Wesley C
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Best Local Similarity 51.1'
Matches 118; Conservative
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SEQ ID NO 8453
LENGTH: 377
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SEQ ID NO 209
LENGTH: 11812
                           Fao, Nengbing
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Best Local Similarity
Matches 68; Conserv
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45.5%; Pred. No. 10;
live 0; Mismatches 152;
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APPLICANT: Cardineau, Guy A.
APPLICANT: Schwab, George E.
APPLICANT: ASCHWab, George E.
APPLICANT: Michaels, Tracy E.
APPLICANT: Michaels, Tracy E.
APPLICANT: Burmelster, Paula
APPLICANT: Dojillo, Joanna
TITLE OF INVENTION: Pesticidal Proteins
FILE REFERENCE: MA-703C2D1
FILE REFERENCE: MA-703C2D1
FRIOR APPLICATION NUMBER: US 09/378,088
PRIOR PLILING DATE: 1999-08-20
PRIOR PLLING DATE: 1999-08-20
PRIOR FILING DATE: 1999-08-20
PRIOR FILING DATE: 1996-04-19
PRIOR FILING DATE: 1996-04-19
PRIOR PELICATION NUMBER: US 08/633,993
PRIOR FILING DATE: 1996-04-19
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OTHER INFORMATION: Undetermined nucleotide.
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OTHER INFORMATION: Undetermined nucleotide.
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OTHER INFORMATION: Undetermined nucleotide
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OTHER INFORMATION: Undetermined nucleotide
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Publication No. US20030106093A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Schnepf, H. Ernest
Knuth, Mark
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SOFTWARE: PatentIn version 3.1
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LOCATION: (68)..(68)
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LOCATION: (73)..(73)
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Best Local Similarity
Matches 127; Conserva
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APPLICANT: POLIARG, Michael R.
APPLICANT: Cardineau, Guy A.
APPLICANT: Schwab, George E.
APPLICANT: Michaels, Tracy E.
APPLICANT: Michaels, Tracy E.
APPLICANT: Michaels, Tracy E.
APPLICANT: Michaels, Tracy E.
APPLICANT: Dojlilo, Joanna
TITLE OF INVENTION: Pesticidal Proteins
FILE REFERENCE: MA-703CD1
CURRENT APPLICATION NUMBER: US/10/099, 278
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: US 08/633, 993
PRIOR PILING DATE: 1999-04-19
PRIOR PLING DATE: 1996-04-19
PRIOR PLLING DATE: 1996-04-19
PRIOR FILING DATE: 1997-04-18
WUMBER OF SED ID NOS: 130
SOFTWARE: PatentIn version 3.1
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 116266
LENGTH: 3290
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Pred. No. 9.5
                                                                                                                                                                                                                                                                                                                                           4.0%; Score 37.2;
59.4%; Pred. No. 6.
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Best Local Similarity 45.5%;
Matches 127; Conservative (
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Matches 63; Conservative
                                                                                                                                                                                                                                                                       ORGANISM: Human
US-10-027-632-116286
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Pred. No. 84;
0; Mismatches
                                                                                                                                       ; Sequence 292, Application US/09764878; Patent No. US20020090615A1; GENERAL INFORMATION:
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Best Local Similarity 49.5%;
Matches 91; Conservative
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                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-878-292
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US-10-079-854-292
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LENGTH: 32038
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                                                                                                                                                                                                         ATATCCAGATGGTCAAACAATTGATGAGGAGGGTAATTTATGGGTTGCCGTTTTCCAAGG 686
                                                                                      AGGTACAGATGAAATAAAAACACAACTAAATGAAGAATTAAAAATAGAATATAGTCATGA 944
AAAAATGCACGAGAGCAACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAA 506
                                                                                                                                                         507 GAAAATGTATTATATTGATTCGGGGAAAAGAAGAGTAGACGAGTACGATTATGATGCTTC
                              705 AAAATATCAATATTGGCAACGAGCAGTAGGAAGTAATGTAGCTTTACGTCCACATGAAAA
                                                                    GAAAATGTATTATATTGATTCGGGGAAAAGAAGAGTAGACGAGTACGATTATGATGCTTC
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45.5%; Pred. No. 13;
iive 0; Mismatches
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FILE REPERENCE: Ma-703C2D1
CURRENT APPLICATION NUMBER: US/10/099,278
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 09/378,088
PRIOR FILING DATE: 1999-08-20
PRIOR FILING DATE: 1996-04-19
PRIOR FILING DATE: 1996-04-19
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PATENTING DATE: 1997-04-18
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 39, Application US/10099278 Publication No. US20030106093A1 GENERAL INFORMATION:
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Knuth, Mark
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Matches 127; Conservative
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17451 TAAAAGGTAAAAACTAAAACCTTTAAGGTGATTCTAAAGGTTCACATGAAAGGCAAAGGG 17510
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                                                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PAL21
CURRENT APPLICATION NUMBER: US/09/764,878
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 4.28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2922
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Publication No. US20030054368A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPRENCE: PA12.C1
CURRENT APPLICATION NUMBER: US/10/079,854
CURRENT FILING DATE: 2002-02-22
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Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 428
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 84;
0; Mismatches 93;
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338 QLYIFKGSHFWEVAADGNVSEPRPLQERWVGLPPNIEAAAVSLNDGDFYFFKGGRCWRFR 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 AFLEKYGYLNEQVPKAPTSTRFSDAIRAFOWVSQLPVSGVLDRATLROMTRPRCGVTDTN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                                                                                                                         Sequence 144, Application US/10123155 Publication No. US20030068794A1 GENERAL INFORMATION:
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                                                                                                              398 GPKPVWGLPQLCRA 411
                                                                     739 GTAAAAATACCAGA 752
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CURRENT APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Godowski, Paul J.
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                                                                                                                                                                                                                                                                                                                                                                                      Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prior Application removed -
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goddard, Audrey
                                                                                                                                                                                                                                                                                              APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                            DeForge, Laura
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                                                                                                                                                                                                                                                                                                                                                                                                          Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang, Zemin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT CORGANISM: Homo Sapien US-10-123-155-144
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Matches 39; Conserva
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                                                                                                                                                                                                      US-10-123-155-144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  559 GATGCTTCTACATTATCCATCAGCAATCAACGCCCATTATTTACTTTTGAAAAGCATGAA 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 FDQDERWSLSRRGRNLFVVLAHEIGHTLGLTHSPAPRALMAPYYKRLGRDALLSWDDVL 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330KH5023
CURRENT APPLICATION NUMBER: US/10/146,731
CURRENT FILING DATE: 2009-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                379 ATTGACGCTGGTCTCCCCGTAGGACCGGTCACTGGCAGTTTATATCATTTAGGGGCTGAT
                                                                                                 CATTATTTACTTTTGAAAAGCATGAAGTGCCTGGATATCCAGATGGTCAAACAATTGATG
           AAAGAAGAGTAGGAGTACGATTATGATGCTTCTACATTATCCATCAGCAATCAACGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - See File Wrapper or Palm
                                                                                                                                                                                                                                                                                                                                              Sequence 144, Application US/10146731
Publication No. US20030129692A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stewart, Timothy A.
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Goddard, Audrey
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Wood, William
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sherwood, Steven
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NUMBER OF SEQ ID NOS: 550
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ORGANISM: Homo Sapien
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                                                                                                      Sequence 2378, Application US/09974300
Fatent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, ID Groth
TITLE OF INVENTION: Marchods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680, 598
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-3-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: PESESEQ for Windows Version 4.0
SEQ ID NO 2378
LENGTH: 630
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3.8%; Score 34.8; Di
Best Local Similarity 48.9%; Pred. No. 14;
Matches 93; Conservative 0; Mismatches
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; ORGANISM: Bacillus licheniformis
US-09-974-300-2378
398 GPKPVWGLPQLCRA 411
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US-09-974-300-2378
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Search completed: August 1, 2003, 14:30:57 Job time: 279 secs

Perfect score: Sequence:

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Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Human NOV5e protei
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Arabidopsis thalia
Drosophila melanog
Sequence gl/32818
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Neisseria meningit
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Z. mobilis aldonol
Staphylococcus epi
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AAW14475
AAY06995
AAB11651
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AAB99723
AAG07424
AAG07423
AAG77423
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281
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N-PSDB; AAF86444.
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 Luciola lateralis
Drosophila melanog
Drosophila melanog
Drosophila melanog
Mouse SMP30 SEQ ID
Rat regucalcin, a
Human ageing marke
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641.269 Million cell updates/sec
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SIDS2/gcgdata/geneseqype-mbl/AA1981.DAT:*

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15: /SIDS2/gcgdata/geneseqyp-embl/AA1991.DAT:*

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18: /SIDS2/gcgdata/geneseqyp-embl/AA1995.DAT:*

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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                         908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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                                                                                                                                                                          WTGTMAIDAGLPVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRR 180
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                                        The present sequence is a firefly protein which regenerates luciferin busing oxyluciferin and D-cysteine. This protein can be used for regeneration of luciferin, a substrate for luciferase, used for APP (adenosine triphosphate) assays in both medical and food hygiene areas.
                                                                                                                                                                                                                                                                                                                                                                                                                             Luciferin regenerating protein; luciferen; oxyluciferin; luminescence;
                                                                                                                                                                                                                                  VDEYDYDASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQP
                                                                                                                                 1 MGPVVEKIAELGKYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSF
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a protein capable of regenerating luciferin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Luciola cruciata-originated genes encoding proteins capable of regenerating luciferin especially from oxyluciferin, for producing
regenerating protein and gene encoding it useful for ing expensive luciferin from oxyluciferin and D-cysteine
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                                                                                                  Length
                                                                                                                 Indels
                                                                                                Score 1615; DB 22;
Pred. No. 8.4e-153;
; Mismatches 0;
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                          Claim 7; Page 16-17; 21pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                             ABB09720 standard; Protein; 309 AA
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                                                                                                  100.0%;
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                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hirokawa K, Kurosawa
                                                                                                                                                                                                                                                                                                              FAGVKVKL 308
                                                                                                                                                                                                                                                                                                     FAGVKVKL 308
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                                                                                                          Similarity
                                                                                  308 AA
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           regenerating
                                                                                                           Local Simines 308;
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 Luciferin
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                                                                                   Sequence
                                                                                                  Query Match
                                                                                                           Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRRVDEYDYDASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKIST
                                                                                                        uciferin. The protein can especially regenerate luciferen from oxyluciferin. The protein can be added to the luciferin-lucifersse reaction system to sustain luminescence and reduce the amounts used. The polynucleotide sequence is useful for producing recombinant transformants, which are useful for the production of proteins useful in assaying ATP in medical sciences and food hygiene.
                                                                                                                                                                                                                                                                                                                                                                                                                1 MGPVVEKIAELGKYTVGEGPHWDHETQTLYFVDTVĖKTFHKYVPSQKKYTFCKVDKLVSF
                                                                                       protein capable of regenerating
                                                                                                                                                                                                                                                                                                                   55.1%; Score 889.5; DB 23; Length 309; 56.6%; Pred. No. 2.8e-80; 1.1ve 47; Mismatches 83; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Luciola lateralis; luciferin; regeneration; Japanese firefly; adenosine triphosphate; ATP; medical science; food hygiene; luciferase; luminescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Luciola lateralis luciferin regenerating protein SEQ ID NO:2.
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                                         Claim 1; Page 18-19; 23pp; Japanese
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recombinant DNAs and transformants
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                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 56.6
Matches 176; Conservative
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                                                                                            present sequence
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N-PSDB; ABL49712.
                                                                                                                                                                                                                                                                              309 AA;
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Venter JC,
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         Luciola lateralis-originated genes encoding proteins capable of regenerating luciferin especially from oxyluciferin, useful for producing recombinant DNAs and transformants to give proteins useful in
                                                                                 The present sequence represents a protein capable of regenerating luciferin, which is isolated from Luciola lateralis (Japanese firefly). The gene encoding the protein capable of regenerating luciferin can be used for producing recombinant DNAs and transformants, which can be used for the production of proteins useful in assaying adenosine triphosphate (ATP) in medical sciences and food hygiene. The protein can be added to the luciferin-luciferase reaction system to sustain luminescence and reduce their amounts used.
                                                                                                                                                                                                                                                            1 MGPVVEKIAELGKYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                            3;
                                                                                                                                                                                                      53.2%; Score 859.5; DB 23; Length 307; 52.8%; Pred. No. 2.7e-77; ive 58; Mismatches 85; Indels 3;
                                                                                                                                                                                                                           Indels
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                                                              Claim 1; Page 18-19; 23pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB63233 standard; Protein; 303 AA.
                                          assaying adenosine triphosphate
                                                                                                                                                                                                                          58;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74
                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insectiods. Therefore in higher eukaryotes for the development of insectiodes, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGITG-ABL30511), expressed DNA sequences (ABLIGITG-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFAGVKVKL 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 VGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDK--LVSFIIPLAGSPGRFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 GPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                    Disclosure; SEQ ID NO 16491; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.2%; Score 568; DB 22; 40.7%; Pred. No. 3.7e-48; ive 48; Mismatches 116;
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Myers EW
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Best Local Similarity 40.7
Matches 121; Conservative
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Adams M,
                                       WPI; 2001-656860/75
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                                                            N-PSDB; ABL07336
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2000US-191637P.
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                                                                                                                      Adams M,
                                                                                                                                          WPI; 2001-656860/75
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Matches 118; Conserv
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WO200171042-A2
                                         23-MAR-2001;
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                                                               23-MAR-2000;
11-JUL-2000;
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                     27-SEP-2001
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                                                                                               detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                            Disclosure; SEQ ID NO 2442; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                       Length 303;
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                                                                                                                                                                                                                                                                                                                     ; Score 550; DB 22;
; Pred. No. 2.3e-46;
48; Mismatches 115;
                                             Myers
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                                              Li PWD,
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  11-JUL-2000; 2000US-0614150
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                                                                                               New isolated nucleic acid genes from Drosophila and interactions
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 39.28
Matches 118; Conservative
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                                              Adams M,
                                                                 WPI; 2001-656860/75.
                        (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                    303 AA;
                                                                             N-PSDB; ABL02653
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                                              Venter JC,
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74 SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV 133
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                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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39.2%; Pred. No. 2.3e-46;
Live 48; Mismatches 115; Indels
Ξ.
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Myers
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Li PWD,
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                                      ABB83787
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                                     ΩD
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                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 GPV----TGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                       developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 26868; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 303;
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Drosophila melanogaster polypeptide SEQ ID NO 26868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 550; DB 22;
Pred. No. 2.3e-46;
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                                                                                                                                                                                                                                 Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.1%;
39.2%;
                                                                                                                                       23-MAR-2001; 2001WO-US09231
                                                                                                                                                                 2000US-191637P.
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                                                           Drosophila melanogaster
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(ABB57737-ABB72072).
                                                                                                                                                                                                                              Adams M,
                                                                                                                                                                                                                                                       2001-656860/75.
                                                                                                                                                                                                     (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 AA;
                                                                                                                                                                                                                                                                   N-PSDB; ABL10795
                                     pharmaceutical
                                                                                    WO200171042-A2
                                                                                                                                                                                                                                                                                                                      interactions -
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                                                                                                                                                                 23-MAR-2000;
                                                                                                                                                                             11-JUL-2000;
                       Drosophila;
                                                                                                              27-SEP-2001
                                                                                                                                                                                                                              JC,
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The invention relates to a senescence marker protein 30 (SMP30) non-human animal having a defect in the SMP30 function. The animals are useful for producing antibody, evaluating its biological function, histopathological diagnosis and onset mechanism of disease due to aging, and in screening side-effects during development of drug and cosmetics including for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 APAVLERHÖGSLYSLFPDHSVKKYFDQVDISNGLDWSLDHKIFYYLDSLSYTVDAFDYDL 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non-human animals with defective senescence marker protein 30 function, useful for producing antibody, histopathological diagnosis and onset mechanism of disease due to aging, and in screening side-effects during
                                                                                                                                                                                                                 senescence marker protein 30; cancer; aging; senescence; SMP30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 YRCGESPVWEEASQSLLFVDIPSKIICRWDTVSNQVQRVAVDAPVSSV--ALRQLGGYVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 36-37; 44pp; Japanese.
ABB83787 standard; Protein; 299 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-2001; 2001WO-JP09243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-2000; 2000JP-0322234
                                                                                                          (first entry)
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                                                                                                                                                            Mouse SMP30 SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kasahara
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nes 112; Conserv
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(KASA/) KASAHARA
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                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                          14-AUG-2002
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03-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW14475;
                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                        122
                                       SMP30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Нишаи
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Op
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                                                                                                                                                                                                                                                                                                                                                                                                                                   123 APAVLERHQGSLYSLFPDHSVKKYFNQVDISNGLDWSLDHKIFYYIDSLSYTVDAFDYDL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237
                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 GPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDA 188
                                                                                                                                                                                                                                                                                                                                                                                          73
                                                                                                                                                                                                                                                                                                                                                                                                         7.1
                                                                                                                                                                                                                                                                                                                                                                                                       14 YRCGESPVWEEASKCLLFVDIPSKTVCRWDSISNRVQRVGVDAPVSSV--ALRQSGGYVA
                                                                                                                                                                                                                                                                                                                                                                                                                        74 SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STLSISNORPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 YTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                                                                                                         A rat liver cDNA clone coding for a calcium binding protein of mol. wt. 33388 was isolated and sequenced (AAQ87295). The protein was designated "regucalcin" (AAR75416).
                                                                                                                                                                                                                                                                 DNA encoding regucalcin – useful for the recombinant production of regucalcin, a calcium binding protein
                                                                                                                                                                                                                                                                                                                                                          Length 299;
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                  .... DB 16; ...
8e-37;
                                                                                                                                                                                                                                                                                                                                                                        121;
                                                                                                                'note= "corresponds to CAA codon"
                                                                                                                                  /note= "corresponds to GAC codon"
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                          28.1%; Score 454.5; 37.5%; Pred. No. 8e-
                                                 Rat regucalcin, a calcium binding protein
                                                                  rat.
                                                                 Calcium binding protein; regucalcin;
                                                                                           Location/Qualifiers
95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR74219 standard; Protein; 299 AA.
¥.
                                                                                                                                                                                                                (DAII-) DAIICHI KAKAGU YAKUHIN KK.
(YAMA/) YAMAGUCHI M.
                                                                                                                                                                                                                                                                                           Claim 1; Page 5-6; 6pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                         41;
standard; Protein; 299
                                                                                                                                                                                  93JP-0279349
                                                                                                                                                                                                 93JP-0279349
                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 37.5
nes 111; Conservative
                                                                                                                                                                                                                                          WPI; 1995-211628/28.
N-PSDB; AAQ87295.
                                                                                                                                                                                                                                                                                                                                           299 AA;
                                                                                                                          Misc-difference
                                                                                                        Misc-difference
                                                                                  Rattus rattus
                                                                                                                                                  JP07123985-A
                                                                                                                                                                                                  09-NOV-1993;
                                 31-JAN-1996
                                                                                                                                                                                  09-NOV-1993;
                                                                                                                                                                  16-MAY-1995
                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189
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AAR75416
                AAR75416;
                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
AAR74219
                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                          qq
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70 REVVSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---TAPAVLERHQGALYSLFPDHHVKKYFDQVDISNGLDWSLDHKIFYYIDSLSYSVDAF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DYDASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 GLPVGPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 GEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKY---TFCKVDKLVSFIIPLAG----SPG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ90035 is the SMP30 gene. It encodes the human ageing marker protein, SMP30 (AAR74219). Human SMP30 is found in human organs, tissues, blood, urine and cerebrospinal fluid. The blood concentration of SMP30 is known to increase with renal and hepatic deficiencies and to decrease with age. It is therefore useful in the monitoring of renal or hepatic deficiencies and for the monitoring of the development of the liver and kidneys in newborn bables.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 GESPVWEEVSNSLLFVD-----IPAKKVCRWDSFTKOVQRVTMDAPVSSVALRQSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptide for detecting human ageing marker protein SMP30 for monitoring liver and kidney development in new-born babies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMP30; senility marker protein; monoclonal antibody; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.8%; Score 448.5; DB 16; Length 36.9%; Pred. No. 3.2e-36; Live 42; Mismatches 113; Indels
                                                                                                               protein; ageing; organ development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     senility marker protein, hSMP30.
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                                                         SMP30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 7-8; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299
                                                            Human ageing marker protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW14475 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                   93JP-0265681
                                                                                                                                                                                                                                                                                                                                                                                                         93JP-0265681
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 110; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-175363/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FJRE ) FUJI REBIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ90035
                                                                                                                                                                                                                                                                                                                                                   29-SEP-1993;
                                                                                                                     marker
                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                    JP07097399-A
                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-1993;
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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions the invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer. remal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---TAPAVLERHQGALYSLFPDHHVKKYFDQVDISNGLDWSLDHKIFYYIDSLSYSVDAF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 RFVVSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYDASTLSISNORPLFTFEKHEVPGYPDGOTIDEEGNLWVAVFQGQRIIKISTQQPEVLL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 DTVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 GLPVGPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 GEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKY---TFCKVDKLVSFIIPLAG----SPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.8%; Score 448.5; DB 20; Length 36.9%; Pred. No. 3.2e-36; ive 42; Mismatches 113; Indels
                                                                                                                                                                                            O'Hare M, Obata Y, Old
Scanlan MJ, Stockert E;
                                                                                                                                                                                                                                                                                                                                                                                                              Example 8; Page 775-776; 787pp; English
                                                                                                                                                  INST CANCER RES
            98US-0102322.
97US-0896164.
97US-0061599.
97US-0061765.
97US-0948705.
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                                                                                                                                                                                            Chen Y, Gout I, Gure A, Pfreundschuh M, Sahin U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110; Conservative
                                                                                                                                                                                                                                                                        WPI; 1999-132448/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 AA;
                                                                                                                                                                                          Gout I,
                                                                                                                                                                                                                                                                                             N-PSDB; AAX40196
                                                                                                                                                      (LUDW-) LUDWIG
                                                                                        10-OCT-1997;
11-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lung cancer
                22-JUN-1998
                                                     10-0CT-1997
                                                                        10-0CT-1997
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                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of human senility marker protein (hSMP30) which has a molecular weight of 30 kDa. Monoclonal antibodies recognising hSMP30 are claimed and can be used in a method for detection of the hSMP30 protein in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 RFVVSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---TAPAVLERHQGALYSLFPDHHVKKYFDQVDISNGLDWSLDHKIFYYIDSLSYSVDAF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 GLPVGPVT-----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 QIVKLPVDKITSCCFGGKNYSEMYVTCARDGMDPEGLLRQPEAGGIFKITGLGVKGIA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer; prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 DTVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GESPVWEEVSNSLLFVD-----IPAKKVCRWDSFTKQVQRVTWDAPVSSVALRQSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYDASTLSISNORPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 GEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKY---TFCKVDKLVSFIIPLAG----SPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                             for
                                                                                                                                                                                                                                                                                             - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 18; Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                         Anti-human senility marker protein monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.8%; Score 448.5; DB 18 36.9%; Pred. No. 3.2e-36;
                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 6-7; 8pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY06995 standard; Protein; 299
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                                                                                                                                95JP-0149791
                                                                                                                                                                     95JP-0149791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                            (FJRE ) FUJI REBIO KK
                                                                                                                                                                                                                                                                                                             detection of protein
                                                                                                                                                                                                                                                 WPI; 1997-073109/07.
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Matches 110; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998;
              Homo sapiens
                                                 JP08319298-A
                                                                                                                                                                     25-MAY-1995;
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                                                                                        03-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Length 299;

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RESULT 12 AAX0699

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Sequences AABI1630-BI1688 represent proteins from Agrobacterium vitis which elicit a hypersensitivity response (HR) in a plant. The invention also relates to nucleotide sequences (AAAG1501-A61524) encoding the A. vitis HR elicitor proteins. The HR is a rapid, localised necrosis that is associated with the active defence of plants against many pathogens, and occurs when a pathogenic organism interacts with a nonhost plant (i.e. one in which intracellular becarial growth and disease development do not occur). Like other HR elicitors, the A. vitis elicitor functions in non-host plants by causing a rapid hypersensitive response that results in walling-off and killing of the pathogen. On grape plants, the A. vitis elicitor induces a restricted necrosis of tissues, resulting in the death of plant cells and induction of pathogen resistance. A. vitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HR elicitor proteins, in non-infectious form, are used to treat plants the lateitor proteins, in non-infectious form, are used to treat plants or their seeds to impart resistance to disease, such as those caused by fund; bacteria or viruses; and to enhance growth, e.g., to increase yield or to provide earlier germination or maturation. The proteins can also be used to control insects, to impart resistance to environmental stresses, e.g., cold, and to import resistance to environmental content. The same effects can be produced by producing transgenic plants or seeds by incorporation of DNA that encodes A. vitis HR elicitor proteins. Ose of A. vitis HR elicitor proteins, or nucleic acids encoding them, may allow control of previously untreatable diseases; provide systemic treatment; and eliminate the need for biological control agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production of
                                            Hypersensitive response elicitor protein; HR; disease resistance;
insecticide; fungicide; antiviral; bactericide; growth enhancer;

    A. vitis hypersensitive response elicitor protein, SEQ ID NO:29.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 104-105; 157pp; English.
                                                                                           stress resistance; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                               Ĥ
                                                                                                                                                                                                                                                                                                                                                                             (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                  99WO-US26079.
                                                                                                                                                                                                                                                                                                                              98US-0107387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a hypersensitive response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or polluting chemicals.
                                                                                                                                       Agrobacterium vitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-376567/32.
N-PSDB; AAA61508.
                                                                                                                                                                                      WO200028056-A2.
                                                                                                                                                                                                                                                                                  05-NOV-1999;
                                                                                                                                                                                                                                                                                                                              06-NOV-1998;
                                                                                                                                                                                                                                   18-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                               Burr TJ,
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74 SLEREIAILTWDGV---SAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAG 130 LPVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDAST 190 LSISNORPLFTFEKHEVPGYPDGQTIDEEGNLWVAVF-----OGQRIIKISTQQP 240 16 VGEGPHWDHETQTLYFVDTVEKTF--HKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV 73 LGEGPTYDVARDTAWWFDILGKGLIEHRFATGE-----TIRHDLPMMAS-ALATI 50; 14.7%; Score 238; DB 21; Length 293; 26.5%; Pred. No. 3.4e-15; ive 46; Mismatches 126; Indels 56 80; Conservative Query Match Best Local Similarity Matches 80; Conserv 17 99 g ò g ò ОР ò ò

293 AA;

Sequence

180 -GLPTGMPTVHIDGRGKDGGIDGAVCDAEGGLWNARWGVGAVDHYDRTGQHLAR----- 232 241 EVLLDTVKIPDPQVTSVAFGGPNLDELHVTSA--GLQLDDSSLDKSLVNGHVYRVTGLGV Hypersensitive response elicitor protein; HR; disease resistance; insecticide; fungicide; antiviral; bactericide; growth enhancer; stress resistance; transgenic plant. A. vitis hypersensitive response elicitor protein, SEQ ID NO:28 AAB11650 standard; Protein; 340 AA. Zhang H; (CORR) CORNELL RES FOUND INC. 98US-0107387. (first entry) Burr TJ, Herlache TC, Agrobacterium vitis. WPI; 2000-376567/32. N-PSDB; AAA61508. 1.1 KG 285 KG 300 WO200028056-A2 06-NOV-1998; 23-OCT-2000 18-MAY-2000. 299 AAB11650; 233 284 RESULT 14 AAB11650 g ò ŏ

New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production of a hypersensitive response

Claim 3; Page 102-104; 1:57pp; English.

Sequences Ambitions represent proteins them which elicit a hypersensitivity response (HR) in a plant. The invention also relates to nucleotide sequences (AAA61501-A61524) encoding the A. vitis HR elicitor proteins. The HR is a rapid, localised necrosis that c. is associated with the active defence of plants against many pathogens, and occurs when a pathogenic organism interacts with a nonhost plant c. is not in which intracellular bacterial growth and disease development of nor occurs. Like other HR elicitors the A. vitis elicitor functions in non-host plants by causing a rapid hypersensitive response that c. results in walling-off and killing of the pathogen. On grape plants, the c. A. vitis elicitor induces a restricted necrosis of tissues, resulting in the elicitor proteins, in non-infectious form, are used to treat plants or the death of plant cells and induction of pathogen resistance. A. vitis elicitor proteins, in non-infectious form, are used to treat plants or their seeds to impart resistance to disease, such as those caused by clungi, bacteria or viruses; and to enhance growth, e.g., to increase yield or to provide earlact germination or maturation. The proteins can also be used to control insects, to impart resistance to environmental content. The same effects can be produced by producing transgenic plants or seeds by incorporation of DNA that encodes A. vitis HR elicitor proteins. Use of A. vitis HR elicitor proteins, and allow control of previously untreatable diseases; provide systemic treatment; and eliminate the need for biological control agents or polluting chemicals. Sequences AAB11630-B11688 represent proteins from Agrobacterium vitis

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                                                                                                                                                                                                       LSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVF-----QGQRIIKISTQQP 240
                                                                                                                                                                                                                                                 EVLLDTVKIPDPQVTSVAFGGPNLDELHVTSA--GLQLDDSSLDKSLVNGHVYRVTGLGV 298
                                                                                                                                                                                                                                                            Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; membrandolesis regulation; tissue growth; anglogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodly characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; neurological disorder; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; wasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.
                                                                        16 VGEGPHWDHETQTLYFVDTVEKTF--HKYVPSQKKYTFCKVDKLVSFIIPLAGSPGREVV 73
                                                                                     131 LPVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDAST
                                                                                                                                                                          SLEREIAILTWDGV---SAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAG
                                                                                                                                                                                                                    50;
                                Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human RNA polymerase-like ORF1018 protein, SEQ ID NO:2036.
                                                    Indels
                             ; Score 238; DB 21;
; Pred. No. 4.2e-15;
46; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                        ABP32045 standard; Protein; 107 AA.
                            h 14.7%;
Similarity 26.5%;
80; Conservative 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAY-2001; 2001WO-US17076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-2000; 2000US-206690P
                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leach MD, Shimkets RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-106200/14.
N-PSDB; ABN76071.
        340 AA;
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                                                   80;
                            Query Match
Best Local Si
Matches 80
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                                                                                                                                       113
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        Sequence
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Considerated ORF (open reading frame) 1-4534, and sequences ABM75054-
ABM79587 represent CDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORF1-ORF4534 (collectively polypeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, olynnucleotides at least 85% identical to polypeptides. The read sequences, vectors and host cells comprising ORFX polynnucleotides. The recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of screening for modulators of ORFX proteins antibodies specific for ORFX proteins, methods of screening individuals for a predisposition to an operative of screening individuals for a predisposition or activity, and methods of screening individuals for a predisposition to an office of screening individuals of the invention have a wide carrivity, and methods of screening individuals for a predisposition to an office of screening individuals of the invention have a wide carrivity and methods of screening individuals of the invention of the carrivity individuals of the involved in the determination of antificative activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. OffX proteins, or ther proliferative disorders such as sporlassis and benign tumours, or theory of and antibodies may be used in the treatment of cancers, or ther proliferative disorders such as sporlassis and antibodies may also be used as a cardiovascular disease, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration of organ transplantation, disorders of tissue growth and regenerate of primers and probes, in the detection of forex genences. In generate dispanses, and infections diseases caused by viral, benefit dispanses, in generate dispanses, and infections of primers, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 DPLGNLWTGTMAIDAGLPVGPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
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Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 KMYYIDSGKRRVDEYDYDASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 IFYXIDSLSYTVXAFDYDLPTGQISNRRTVXKMEKDE--QIPDGMCIDVEGKL 107
                                                                                                                                                                                                                                                                                                                                Sequences ABP31028-ABP35561 represent 4534 novel human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
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43.4%; Pred. No. 1.3e-11;
iive 9; Mismatches 44
                                                                                                                                                                                                                                       Claim 10; Page 773; 2508pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.1
Best Local Similarity 43.4
Matches 49; Conservative
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 1, 2003, 14:31:08; Search time 37 Seconds (without alignments) 800.254 Million cell updates/sec

US-10-089-986-2 1615 1 MGPVVEKIAELGKYTVGEGP..........HVYRVTGLGVKGFAGVKVKL 308 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		•			SUMMARIES	
Result		Olerv				
NO.	Score	Match	Length	DB	ID	Description
1	550	34.1	303	7	JC7250	anterior fat bodv
7	538	33.3	306	7	JC7249	fat
3	457.5	28.3	299	7	S72173	ce ma
4	454.5	28.1	299	~	S34588	senescence marker
Ŋ	448.5	27.8	299	-	560035	
9	423.5	26.2	569	7	E95309	probable calcium b
7	409.5	25.4	260	7	AI3216	hypothetical prote
80	376	23.3		-	A70047	က
თ	365.5	22.6		7	B90445	requialin homolog
10	331	20.5		~	A87351	. Smp-30/Cgrl family
11	315	19.5		~	A87473	Smp-30/Cgrl family
12	292	18.1		7	G90485	>
13	288.5	17.9		~	D95265	probable requcalci
14	273	16.9		7	AB3071	calcium-binding pr
15	273	16.9		~	G98215	senescence marker
16	256	15.9		~	AH2662	calcium-binding pr
17	256	15.9		7	G97444 ·	probable calcium-b
18	206	12.8		7	AF3043	calcium-binding pr
19	206	12.8		~	F98242	regucalcin (ABÕ379
20	203	12.6		7	AH0832	conserved hypothet
21	202.5	12.5		7	AG3501	gluconolactonase (
22	153.5	9.5		7	AH3051	gluconolactonase p
23	153.5	9.5	348	7	D98234	probable gluconola
24	140	8.7		7	C95896	
25	132	8.2		7	G95274	probable gluconola
26	124.5	7.7		7	S28218	
27	120	7.4		7	B87401	gluconolactonase [
28	113	7.0	303	7	10	
29	111	6.9	356	7	D82643	conserved hypothet

RESULT 2 JC7249 anterior fat body protein - flesh fly (Sarcophaga peregrina)

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Drp35 protein - St protein Y76A2A.2 (copper-transportin	conserved hypothet Drp35 [imported] - exopolygalacturona	hypothetical prote mucin-like protein	procession probabile transamin hypothetical integ	nypornerical proce mucin-like protein hemicentin precurs	probable exported translation elonga
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ALIGNMENTS

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RESULT 1 C.Species: Drosophila sp. S.Accession: JC720 N. Hall and Company of the sp. A. Accession: JC720 A. Molecule type: MRN A. Accession: JC720 A. Molecule type: MRN A. Accession: JC724 A. Accession: JC744 A. Accession: JC7

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Nalternate mannes: required mannes: Rattus norvegicus (Norway rat)

C; Species: Rattus norvegicus (Norway rat)

C; Accession: S34589; S34589; S37203

R; Shimokawa, N.; Yamaquchi, M.

FRES Lett. 327, 251-253, 1993

A; Title: Molecular cloning and sequencing of the cDNA coding for a calcium-binding pr
A; Reference number: S34588; MUID:93351639; PMID:8348951

A; Reference number: S34588; MUID:93351639; PMID:8348951

A; Residues: 1-299 < SHID

A; Cross-references: GB:D38467; GB:D16386; NID:g600378; PIDN:BAA07490.1; PI
A; Status: preliminary

A; Status: mRNA
A; Residues: B4-299 < SHID
A; Cross-references: EMBL:D14327

A; Cross-references: EMBL:D14327

B; Fujita: T; Shirasawa, T; Uchida, K; Maruyama, N.
Biochim: Biophys: Acta 1132, 297-305, 1992

A; Title: Isolation of cDNA clone encoding rat senescence marker protein-30 (SMP30) an A; Reference number: S27203; MUID:93041931; PMID:1420310

A; Status: preliminary
A; Status: prelimina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 GPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 STLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLDT 246
                                                                                                                                                                                                                                                                                                      74 SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV 133
                                                                                                                                                                                                                                                                                                                                          GPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 YTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 VKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
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A; Residues: 1-147, 'D', 149-299 <FUJ>
A; Cross-references: EMBL:X69021; NID:g57254; PIDN:CAA48786.1; PID:g57255
C; Superfamily: senescence marker protein-30
C; Keywords: calclum binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 299;
                                                    Length 299;
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                                                    28.3%; Score 457.5; DB 2;
llarity 37.8%; Pred. No. 1.9e-29;
Conservative 40; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               senescence marker protein SMP-30 - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 28.1%
Best Local Similarity 37.5%
Matches 111; Conservative
C; Keywords: calcium binding
                                                                                         Best Local Similarity
Matches 112; Conserv
                                                              Query Match
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C;Accession: S72173; S72174 ...
C;Accession: S72173; S72174 ...
B;Fujita, T.; Shirasawa, T.; Maruyama, N.
Biochim. Biophys. Acta 128, 49-57, 1996 A;Title: Isolation and characterization of genomic and cDNA clones encoding mouse senesch. A;Reference number: S72173; MUID:96328264; PMID:8765750
                                                                                                                                                                                                                                                                                                                          A; Experimental source: larval fat body
A; Accession: PC7071
A; Molecule type: protein
A; Residues: 157-168;174-185;186-195 <NA2>
C; Comment: This protein, a homolog of the senescence marker protein-30, has its function C; Genetics:
   C;Species: Sarcophaga peregrina
C;Species: Og-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C;Accession: JG7249; PC7071
R;Nakajima, Y; Natori, S.
A; Blochem. 127, 901-908, 2000
A;Title: Identification and characterization of an anterior fat body protein in an insect A;Reference number: JG7249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STQQPEVLLDTVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 NPTTGKVLLE-IKFPCKQITSAAFGGPNLDILVVTTS-----SRFGEPDPAGTTYKVTG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IIPLAGSPGRFVVSLEREIAILTWDGVSAAPTSIEAIVNV---EPHIKNNRLNDGKADPL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 KRRVDEYDYDASTLSISNQRPLFTFEKHEVPGY--PDGQTIDEEGNLWVAVFQGQRIIKI 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 GNLWTGTMAIDAGLPVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSG 177
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A; Residues: 1-299 <FUU>
A; Cross-references: EMBL:U28937; NID:g1143999; PIDN:AAC52721.1; PID:g1144000
A; Accession: S72174
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: 1-54 <FUN>
A; Cross-references: EMBL:U32170; NID:g1144337; PIDN:AAD03478.1; PID:g1144338
A; Cross-references: Liver
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 PVVEKIAELGKYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKV--DKLVSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 PLPDSHAEL----GEGPHWDVATQNLYYVDINAGKLLRYNYNENKVYKAKIEGEDLAGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Match 33.3%; Score 538; DB 2; Length 30 Local Similarity 39.0%; Pred. No. 6.1e-36; Local Similarity 48; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: calcium binding
A; Note: age-associated decrease
C; Superfamily: senescence marker protein-30
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C;Superfamily: senescence marker protein-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        senescence marker protein 30 - mouse
                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-306 <NAK>
A; Cross-references: DDBJ:AB036903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     II II: |::|
LGAKGYPMTKIQL 306
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                                                                                                                                                                                                                                A; Accession: JC7249
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Best Local Si
Matches 122;
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A; Accession: AI3216
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                                                                                                                                                                                                  A;Gene: SMa0717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
                                                                                                                                                                                      C; Genetics:
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                                                                                                                                                                                                           Senescence marker protein 30 - human
N.Alternate names: regucalcin
S.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
S.Species: Homo sapiens (man)
A.Title: Isolation of cDNA clone encoding human homologue of senescence marker parketence number: IS2491; MUID:96004897; PMID:7548213
A.Reference number: IS2491; MUID:96004897; PMID:7548213
A.Residues: 1-299 <FUJS
A.Residues: 1-299 <FUJS
A.Residues: REMBL:D31815; NID:91072311; PIDN:BAA06602.1; PID:91072312
C.Genetics:
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6
                                  246
                                                70 RFVVSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYVATIGTKFCALMWKEQSAV----VLATVDNDKKNNRFNDGKVDPAGRYFAGTMAEE- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---TAPAVLERHQGALYSLFPDHHVKKYFDQVDISNGLDWSLDHKIFYYIDSLSYSVDAF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYDASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLL 244
APAVLERHQGSLYSLFPDHSVKKYFNQVDISNGLDWSLDHKIFYYIDSLSYTVDAFDYDL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLPVGPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLDT
                                                                                                 VKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 GEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKY---TFCKVDKLVSFIIPLAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 448.5; DB 1;
Pred. No. 1e-28;
42; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GDB:9955055
A;Map position: Xpl1.3-Xpl1.2
C;Superfamily: senescence marker protein-30
C;Keywords: calcium binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.8%;
36.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 27.89
Best Local Similarity 36.99
Matches 110; Conservative
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-569 < KUR>
                                                                                             247
123
                                                                183
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Species: Agrobacterium tunefaciens
C; Decies: Agrobacterium tunefaciens
C; Date: 11.3an-2002 #sequence_revision 11.3an-2002 #text_change 11.3an-2002
R; Mccession: Al301-2002 #sequence_revision 11.3an-2002
R; Mcod, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
A;Cross-references: GB:AE006469; PIDN:AAK65039.1; PID:g14523470; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F:, Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science, 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner S.; Wells, D.H.; Wong, K.; Yeh, A;Teference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein Atu5464 [imported] - Agrobacterium tumefaciens (strain C58, Dupo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-560 <KUR>
A;Cross-references: GB:AE008687; PIDN:AAL46151.1; PID:g17743920; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342
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394 SMRLDVSRP----TGSLYRLTSAGEVTRAGSGFTVANGLAWSPDSSTFYFVDTVPGIIYA
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regucalcin homolog [imported] - Sulfolobus solfataricus
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C; Species: Species: R; Species: Bacillus Species: Species: R; Species
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A:Experimental source: strain 168
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                                                                                 VGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLS 192
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----TGALYRINANGASERKEGGIIVSNGLGWSPDGRTFYFVDTVPGLIHAYDCDPATGA
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C; Species: Sulfolobus solfataricus
C; Species: Sulfolobus solfataricus
C; Species: Sulfolobus solfataricus
C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C; Date: 20-May-2001 #sequence_revision 2001
C; Date: 24-May-2001 #sequence_revision 2001
C; Shepsin 25 A.; Sensen, C.W.; Wadina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Wan der Oost, J.
Submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Accession: B90445
A; Reference B90445
A; Status: preliminary
A; Residues: 1-285 cKUR>
A; Cross-references: GB:AE006641; NID:g13816023; PIDN:AAK42817.1; GSPDB:GN00155
C; Superfamily: senescence marker protein-30
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C;Genetics:
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                                       Score 331; DB 2;
Pred. No. 3.1e-19;
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RGLQNFRFKI 284
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Local Similarity
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Matches 98; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CC0820
C; Superfamily:
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Conserved hypothetical protein [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C;Species: G94885
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Ch. Jong, II.; Jefffris, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: G90485
A;Accession: G90485
A;Status: preliminary
A;Residues: 1-285 <KUR>
A;Residues: 1-285 <KUR>
A;Residues: 1-285 <KUR>
A;Cross-references: GB:AE006641; NID:g13816441; PIDN:AAK43142.1; GSPDB:GN00155
C;Genetics: So3041
C;Superfamily: senescence marker protein-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 NDGKADPLGNLWTGTMAIDAGLPVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 KIAELGKY--TVGEGPHWDHETQTLYFVDTVEK--TFHKYVPSQKKY-----TFCKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KMYYIDSGKRRVDEYDYDASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.1%; Score 292; DB 2; 30.1%; Pred. No. 4.3e-16; tive 50; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 85; Conserv
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    RESULT 12
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Smp-30/Ggrl family protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: A87473
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shaphro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Scaus: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247
        10;
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                            72 VVSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 VGPVTGSLYHLGADKKVKMHESN-IAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
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                                                                                                                                                        67
                                                                                                                    SISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLLDTVKIPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EREIAILTWDGVSAAPTSI-EAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAI--DAGLP
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                                                                                                                                                                                                                                                                                132 PVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYXIDSGKRRVDEYDYDASTL
            Gaps
        20;
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30.9%; Pred. No. 6.2e-18;
.ive 51; Mismatches 115; Indels
        Indels
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C;Superfamily: senescence marker protein-30
47;
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Best Local Similarity 30.94
Matches 93; Conservative
        Conservative
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16.9%;
31.1%;
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Best Local Similarity 31.1%
Matches 82; Conservative
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Job time : 41 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ster E.W.
Aritle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
A;Reference number: AB2577; PMID:11743193
A;Accession: AB3071
                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: prelinioary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-293 <KUR>
A; Cross-references: GB: AE008689; PIDN: AAL44984.1; PID: 917742642; GSPDB: GN00187
A; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 RFVVSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLPVGPVTGSLYHLGADKKV-KMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDÄ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |----AGRLMHLIELPASWPTSCTFGGPVLSTLYVTSARFTWTGDHLDMHPLEGGLFAVE 286
                                                                                                                                                                                                                                                                                     68 FIVGLSRNVCLWTPDG-----PFEEFAMPEPDLPENRLNEGRVAPDGSFWVATMOSNLD 121
                                                                                                                                                                                                                                                                                                                            AG---LPVGPVTGSLYHLGADKKV-KMHESNIAIANGLAWSNDLKKMYYIDSGKRKVDEY 184
                                                                                                                                                                                                                                                                                                                                                                                                              DYDASTLSISNQRPLFT-FEKHEVPGYPDGQTIDEEGNLW-----VAVFQGQRIIK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                        235 ISTQQPEVLLDTVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVT 294
                                                                                                                                                                                                                                                FVVSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMA--ID 128
                                                                                                                                                              13 KYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAG--SPGR 70
                                                                                                                                                                                        12 KDIVGESILMCGDERALYWVDIVGKRIHRLEPENGRHDTWPTPDFVTSI----GMRKDGG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 VGESPTWDERTGDLWFVDILAPAIFCLSPS------GKLQRFDMPAQIGCLGLCQSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 VGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPL-AGSPG----
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                                                                                                                       43;
                                                                              Length 311;
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                                                                                                                       Indels
                                                                              17.9%; Score 288.5; DB 2; 28.1%; Pred. No. 9.4e-16;
                                                                                                                       47; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Map position: linear chromosome C;Superfamily: senescence marker protein-30
A;Gene: SMa0060
A;Genome: plasmid
C;Superfamily: senescence marker protein-30
                                                                                                                           85; Conservative
                                                                                                 Best Local Similarity
Matches 85; Conserv
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GVG 289
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Best Local S:
Matches 82
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Seriescence marker protein-30 (AB03336B) [imported] - Agrobacterium tumefaciens (strail c) Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 15-Feb-2002
C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 15-Feb-2002
C; Accession: G98215
B; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-232B, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A; Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-322 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK89249.1; PID:g15159075; GSPDB:GN00170
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 GLPVGPVTGSLYHLGADKKV-KMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPE-VLLDTV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 VGESPTWDERTGDLWFVDILAPAIFCLSPS-----GKLQRFDMPAQIGCLGLCQSN 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 QTGRLGPAKRLHDFQPDE--GRPDGAATDSEGCYWSAGVQAGRLNRFT---PDGELFEIY 267
                              STLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWYAVFQGQRIIKISTQQPE-VLLDTV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 VGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPL-AGSPG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 273; DB 2;
Pred. No. 1.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: AGR_L_1336
A;Map position: linear chromosome
C;Superfamily: senescence marker protein-30
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                                                                                                                                                              KIPDPQVTSVAFGGPNLDELHVTS 271
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 1, 2003, 14:25:59; Search time 22 Seconds (without alignments) 580.669 Million cell updates/sec Run on:

Title:

Perfect score: Sequence:

US-10-089-986-2 1615 1 MGPVVEKIAELGKYTVGEGP..........HVYRVTGLGVKGFAGVKVKL 308

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_40:* Database :

SUMMARIES

		dЬ			SUMMARIES		
Result		Query					
No.	Score	Match	Length DB	DB	σı	Q.	
1	459	28.4	299	ч	SM30_RABIT	Q9ttj6 oryctolagus	laqus
7	457.5	28.3	299	1	SM30_MOUSE		musculu
m	454.5	28.1	299	П	SM30_BOVIN	pos	taurus
4	454.5	28.1	299	П	SM30_RAT	ratt	norv
ហ	448.5	27.8	299	Н	SM30_HUMAN		apien
9	391.5	24.2	275	7	Y31K_SULAC		opas
7	376	23.3	292	П	YVRE_BACSU		ns sn
80	235	14.6	340	7	CGR1_CANAL		a alb
б	124.5	7.7	320	٦	GNL_ZYMMO		nas m
10	100		358	Н	YBQ3_YEAST		romyc
11	94.5		409	~	EFTU_CHLVU		llav
12	94	5.8	401	Н	PGK_HALVA		cula
13	92.5	5.7	4351	ч	FAT2_RAT		norv
14	95	5.7	4349	ч	FAT2_HUMAN	Q9nyq8 homo sapien	apien
15	91.5	5.7	242	7	RL1_STRVG		omyce
16	91.5	٠	663	Н	ABA2_NICPL		ana p
17	91	5.6	968 .	٦	XYNA_BACHD	P07528 bacillus	us ha
18	91		268	7	FTS1_BUCAP	085297 buchnera ap	ra ap
19	90.5	•	242	7	RL1_STRSQ		omyce
20	90.5		539	Н	CH61_BRAJA		hizob
21	90.5		545	Н	CH63_BRAJA		hizob
22	89.5	5.5	387	П	XYLA_THETH		s the
23	88	٠	892	-	LDL2_XENLA		s lae
24	88.5	•	294	П	OCCT_RHIME		ium m
25	88.5	•	431	Н	SPAL_SALTY	P39444 salmonella	ella
56	88	5.4	922	Н	DPO1_RICFE	Q9raa9 rickettsia	tsia
27	87.5	5.4	242	~	RL1_STRAU		ошусе
28	87.5	5.4	862	~	LOX1_HORVU		m vul
29	87	5.4	745	Н	RNR_BUCAI	P57628 buchnera	ra ap
30	87	5.4	1071	П	CARB_BACSU		
31	86.5	5.4	720	П	VP19_BPAPS	Q9t1s9 bacteriopha	iopha
32	98	5.3	405	٦	DHMH_METME		ophil
33		5.3	350	1	RLAO_HALVO	P41198 halobacter	cteri

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salmonella	saccharomyc	mycobacteri	homo sapien	drosophila	escherichia	mycoplasma	rattus norv	staphylococ	mus musculu	saccharomyc
006973	P52488	053339	P53396	09bi17	P46883	049413	P98158	008854	P11835	P32074
IC_SALMO	A2_YEAST	33_MYCTU	JY_HUMAN	L_DROYA .)_ECOLI	11_MYCGE	22_RAT	50_STAAU	32_MOUSE	C_YEAST
1 FL:	1 UB/	1 YV	1 AC	1 YE	1 AMC	1 HMI	1 LRI	1 CH(1 IT	1 COI
504	636	992	1101	541	757	1139	4660	538	771	935
5.3	5.3	5.3	5.3	5.5	2.5	5.5	5.5	5.2	5.5	5.2
82	82	82	82	84.5	84.5	84.5	84	83.5	83.5	83.5
	1 FLIC_SALMO Q06973	1 FLIC_SALMO 006973 1 UBA2_YEAST P52488	1 FLIC_SALMO 006973 1 UBA2_YEAST P52488 1 YV93_MYCTU 053339	1 FLIC_SALMO 006973 1 UBA2_YEAST P52488 1 V93_3_WYCTU 053339 1 ACLY_HUMAN P53396	5.3 504 1 FLIC_SALMO 006973 5.3 636 1 UBA2_YEAST P52488 5.3 992 1 YV93_MYCTU 053396 5.3 1101 1 ACLY_HUMAN P53396 5.2 541 1 YELL_DROYA . 09bi17	5.3 504 1 FLIC_SALMO 006973 5.3 636 1 UBA2_YEAST 053488 5.3 992 1 YV93_MYCTU 053339 5.3 1101 1 ACLY_HUMAN P53396 5.2 541 1 YELL_DROYA . 09bil7 5.2 757 1 AMO_ECOLI P64883	5.3 504 1 FLIC_SALMO 006973 5.3 636 1 UBA2_YEAST P52488 5.3 992 1 YV93_MYCTU 053339 5.3 1101 1 ACLY_HUMAN P53396 5.2 757 1 AMO_ECOLI P68883 5.2 1339 1 HWM1_MYCGE 049413	5.3 504 1 FLIC_SALMO Q06973 5.3 636 1 UBA2_VESST P52488 5.3 992 1 YV93_MYCTU Q53339 5.3 1101 1 ACLY_HUMAN P53366 5.2 541 1 YELL_DROYA Q9bil7 5.2 139 1 HMMI_MYCGE Q4813 5.2 4660 1 LRP2_RAT P98158	5.3 504 1 FLIC_SALMO 006973 5.3 656 1 UBA2_YEAST 053349 5.3 992 1 YY93_AYCTU 053339 5.3 1101 1 ACLY_HUMAN P53396 5.2 541 1 YELL_DROYA . 09bil7 5.2 757 1 AMO_ECOLI P64833 5.2 1660 1 LRP2_RAT P98158 5.2 538 1 CH60_STAAU 008854	85 5.3 504 1 FLIC_SALMO Q06973 salmonella 85 5.3 963 1 WBA2_FRAST P52488 saccharomyc 85 5.3 10 1 ACLY_HUMAN P53396 homo sapien 84.5 5.2 541 1 YELL_DROYA Q9bil7 crosophila 84.5 5.2 1139 1 HMW1_MYGE Q49413 mycoplasma 84 5 2 1139 1 HMW1_MYGE Q49413 mycoplasma 84 5 2 460 1 LRP2_RAT P98158 ratuus norv 83 5 2 77 1 ATP2_MOUSE P11835 mutus musculu 83 5 2 77 1 ATP2_MOUSE P11835 mutus musculu

ALIGNMENTS

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		ż	celeostomi	conserved	MATIC ACT SULATION O	wugh a col	299; ts 28;	IPLAGSPGRF : ALRKSGGY	rgtmaidagl GTMAEE	KRRVDEYDY : AYSVDAFDY	QQPEVLL
		lcin) (RC)	brata; Eut yctolagus.	is highly	ON OF ENZY THE DYSREC IMILARITY) ilarity). FAMILY.	duced threes and the are no 1 its conteursage by tp://www.i	<pre>bB CRC64; ; Length 299; 9; 16; Indels</pre>	KVDKLVSFIJ : : : TMDAPVTSV	KADPLGNLW1 : KVDPAGRYF2	LKKMYYIDSC KIFYYIDSI	QGQRIIKIST
ALIGNMENIS	299 AA.	DYFIUS: 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Senescence marker protein-30 (SMP-30) (Regucalcin)	Kosn VI SMESO. Oryctolagus cuniculus (Rabbit). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	ILI SEQUENCE FROM N.A. TISSUE-Liver; MEDLINE-20351777; Pubmed=10891565; Misawa H., Yamaguchi M.; "The gene of Ca2+-binding protein regucalcin is highly conserved	VericeDates Species. 1nt. J. Mol. Med. 6:191-196(2000). -!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF ENZYMATIC ACTIVITY IN THE LIVER. DECREASE OF SMP30 LEADS TO THE DYSREGULATION OF CALCIUM SIGNALING IN THE AGED LIVER (BY SIMILARITY). -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity). -!- SIMILARITY: BELONGS TO THE SMP-30 / CGRI FAMILY.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it mose by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce send an email to license@isb-sib.ch). EMBL: AB035445; BAA88079.1;	33108 MW; A8F94AD6595A0C68 CRC64; 28.4%; Score 459; DB 1; Length 29: 38.1%; Pred. No. 2.9e-29; tive 41; Mismatches 116; Indels	GEGPHWDHETQTLXFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVVSLE	REIAILIWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPVGPV :	TGSLYHLGADKKVKMHESNIAIANGLAMSNDLKKMYYIDSGKRRVDEYDYDASTL 	SISNORPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLLDTVKI
ארדסו	PRT;	Created) Last sequence update) Last annotation updat ein-30 (SMP-30) (Regu	bit). ta; Crania rpha; Lepo	0891565; protein re	6(2000). OLE IN THE OF SMP30 HE AGED LI CYTOPlasmi THE SMP-3	opyright. te of Biois s Institut tutions as t is not a e agreemer	MW; ABF94 ; Score 4 ; Pred. 1 41; Misn	TVEKTFHKYN :: IPGKKFCRWN	IEAIVNVEPH : : : VVALATVDKI	VKMHESNIA: : : : VKKYFDQVD	GYPDGQTID
	STANDARD;	41, Created) 41, Last seg 41, Last ann protein-30 (). cuniculus (Rabbit) (etazoa; Chordata; ttheria; Lagomorpha 1986;	YOM N.A. S51777; PubMed=1 Yamaguchi M.; of Ca2+-binding	S."; 6:191-19 PLAY A RU DECREASE LING IN TI OCATION: ELONGS TO	ntry is controlled in institution of institution it institutions in institution i	ro ro	ETQTLYFVD: :: ASGSLLFVD:	DGVSAAPTS : EDQS	LYHLGADKK : LYALFPDHQ	FTFEKHEVP
		002 (Rel. 002 (Rel. 002 (Rel. ce marker	SMF30. agus cunicita; Metazos a; Eutheria	SEQUENCE FROM N.A. TISSUE-liver; MEDLINE-20351777; Pubmed=10891565; Misawa H., Yamaguchi M.; "The gene of Ca2+-binding protein	Le Specie: Mol. Med. TION: MAY HE LIVER. IUM SIGNA! ELLULAR L	This SWISS-PROT entry is copyribetween the Swiss Institute of the European Bioinformatics Insuse by non-profit institution modified and this statement is entities requires a license agor send an email to license@isj. Send. AB033445; BAA88079.1; Calcium-binding.	CE 299 AA Ch . 11 Similarity 114; Conse				
	SM30_RABIT ID SM30_RABIT	15-JUN-2002 15-JUN-2002 15-JUN-2002 Senescence m	KGN OK SMF30. Oryctolagus cuni Eukaryota; Metaz Mammalia; Euther NCBI_TaxID=9986;	SEQUENCE FROM TISSUE=Liver; MEDLINE=20351 Misawa H., Ya "The gene of	Int. J. J Int. J. J IN T CALC	This SWI between the Euro use by modified entities or send 	SEQUENCE 299 AA; Query Match . Best Local Similarity Matches 114; Conserv	17	77	137	192
	RESULT SM30_RI ID SN	25 E E E E	S 0 0 0 2	R R R R R R R R R R R R R R R R R R R	Z Z 8 8 8 8 8 8 8	38888888888 ≋	SO DO Wasi	Qy	Qy	Oy DD	Qy

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 REIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPVGPV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 VLERRQGSLYSLEPDHHVEXYEDQVDISNGLDWSMDHKIFYYIDSLSYSVDAFDVDLQTG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SISNORPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLDTVKI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTL 191
                                                                                                                                                                      STLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLLDT 246
:: : | |: : | |: | TIGTKFCALNWEN-----QSVFVLAMWDEDKKNNRFNDGKVDPAGRYFAGTMAEE----T 122
                                                                          GPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDA 188
                                                                                                 123 APAVLERHQGSLYSLFPDHSVKKYFDQVDISNGLDWSLDHKIFYYIDSLSYTVDAFDYDL 182
                                                                                                                                                                                                  183 QTGQISNRRIVYKMEKDE--QIPDGMCIDABĞKLMVACYNGGRVIRL---DPETGKRLOT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 GEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVVSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 GESPVWEEASNSLLFVDIPAKKVCRWDSLSKQVQRVTVDAPVSSV--ALRQSGGYVATVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misawa H., Yamaguchi M.;
"The gene of Ca2+-binding protein regucalcin is highly conserved in vertebrate species.";

Int. J. Mol. Med. 6:191-196(2000).

Int. J. Mol. Med. 6:191-196(2000).

IN THE LIVER. DECREASE OF SMP30 LEADS TO THE DYSREGULATION OF CALCIUM SIGNALING IN THE SED LIVER (BY SIMILARITY).

INTELLIVER. DECREASE OF SMP30 LIVER (BY SIMILARITY).

INTELLIVER. LOCATION: Cytoplasmic (By similarity).

INTELLIVER. DECREASE TO THE SMP-30 / CGRI FAMILY.
                                                                                                                                                                                                                                                                     247 VKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Senescence marker protein-30 (SMP-30) (Regucalcin) (RC).
RGN OR SMP30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 AA; 33308 MW; 4258F7CDB3CCB575 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.1%; Score 454.5; DB 1; 38.1%; Pred. No. 6.6e-29; iive 38; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20351777; PubMed-10891565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB035446; BAA88080.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovidae; Bovinae; Bos.
NCBL_TaxID=9913;
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Matches 111; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                  134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A MUTATALE LY, Yamaguchi M.;

A Mutata T., Yamaguchi M.;

E Molecular cloning of the CDNA coding for regucalcin and its mRNA expression in mouse liver: the expression is stimulated by calcium administration..;

Li Mol. Cell. Biochem. 173:127-133(1997).

II. Mol. Cell. Biochem. 173:127-133(1997).

IN THE LIVER. DECREASE OF SMP30 LEADS TO THE DYSREGULATION OF CALCIUM SIGNALING IN THE REGULATION OF CALCIUM SIGNALING. THE AGED LIVER.

C -1- SUBCELLUIAR LOCATION: Cytoplasmic.

C -1- TISSUE SPECIFICITY: MAINLY PRESENT IN THE LIVER. WEAK EXPRESSION WAS FOUND IN THE BRAIN AND LUNG, NOT FOUND IN THE KIDNEY.

C -1- DEVELOPMENTAL STAGE: PROTEIN AMOUNTS IN LIVER DECREASE

SIGNIFICANTLY WITH AGE.

C -1- SIMILARITY: BELONGS TO THE SMP-30 / CGRI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 YRCGESPVWEEASQSLLEVDIPSKIICRWDTVSNQVQRVAVDAPVSSV--ALRQLGGYVA 71
          14 YTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV 73
                                                                                  PDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKG----FAG 303
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujita T., Shirasawa T., Maruyama N.; Isolation and characterization of genomic and cDNA clones encoding muse senescence marker protein-30 (SWF30)."; Blochim. Blophys. Acta 1308:49-57(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
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                                                                                                                                                                                                                                                      SM30_MOUSE STANDARD; PRT; 299 AA.
064374; Q60944;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Senescence marker protein-30 (SMP-30) (Regucalcin) (RC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Liver;
MEDLINE-96328264; PubMed-8765750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97422495; PubMed-9278263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U28937; AAC52721.1; -. EMBL; U32170; AAD03478.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-2DPAGE; Q64374; MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Calcium-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D86217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Simi
hes 112;
                                                                                                                                                                                                                                                                                                                                                                                                                RGN OR SMP30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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FOUND IN 5-DAY-OLD NEONATES. EXPRESSION INCREASES FROM DAY 7 AND REACHES A PLATEU AT DAY 10. 3-6.5 MOTH-OLD ADULTS EXPRESS ABOUT A HIRD THE AMOUNT OF NEONATES LEVEL. IN KIDNEY, EXPRESSION INCREASES FROM DAY 21 AND REACHES A MAXIMAL LEVEL AT DAY 35, REMAINS HIGH UNTIL 3 MONTHS OF AGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shimokawa N., Matsuda Y., Yamaguchi M.; "Genomic cloning and chromosomal assignment of rat regucalcin gene."; Mol. Cell. Blochem. 151:157-163(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mech. Ageing Dev. 87:219-229(1996).
-!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF ENZYMATIC ACTIVITY IN THE LIVER. DECREASE OF SMP30 LEADS TO THE DYSREGULATION OF CALCIUM SIGNALING IN THE AGED LIVER.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: HEPATOCYTES AND RENAL PROXIMAL TUBULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMP30): coordinated
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE: IN LIVER, THE FIRST PEAK OF EXPRESSION WAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimokawa N., Yamaguchi M.;
"Molecular cloning and sequencing of the cDNA coding for a calcium-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Wistar; TISSUE-Liver;
MEDLINE=93041931; PubMed=1420310;
MIDIANE=93041931; PubMed=1420310;
MIDIANE=93041931; PubMed=1420310;
"Isolation of cDNA clone encoding rat senescence marker protein-30 (SMP30) and its tissue distribution.";
Biochim. Biophys. Acta 1132:297-305(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY.

PUBLINE-96386712; PubMed-8794449;

Pujita T., Shirasawa T., Uchida K., Maruyama N.;

Fujita T., Shirasawa T., Uchida K., Maruyama N.;

"Gene regulation of senescence marker protein 30 (SMP30): coordin up-regulation with tissue maturation and gradual down-regulation
                                                         PDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKG 300
                                                                                   SM30_RAT STANDARD; PRT; 299 AA.
003336; 033496; 01-0CT-1993 (Rel. 27, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Senescence marker protein-30 (SMP-30) (Regucalcin) (RC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: THE N-TERMINUS IS BLOCKED.
SIMILARITY: BELONGS TO THE SMP-30 / CGR1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from rat liver.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Sprague-Dawley; TISSUE-Kidney;
MEDLINE-96150990; PubMed-8569761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Wistar; TISSUE=Liver;
MEDLINE=93351639; PubMed=8348951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binding protein regucalcin fro
FEBS Lett. 327:251-255(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 117-299 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPITHELIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with aging."
                                                                                                                                                                                                                                                                                                                           RGN OR SMP30
                                                         250
                                                                                                                                                             RESULT 4
                                                                                                                                                                                   SM30_RAT
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                                                                                                                                                                                                                                                                                                                                              72 TIGTKFCALNWE-----DQSVFILAMVDEDKKNNRFNDGKVDPAGRYFAGTMAEE---T 122
                                                                                                                                                                                                                                                                                                                                                                                   GPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDA 188
                                                                                                                                                                                                                                                                                                                                                                                                     SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV 133
                                                                                                                                                                                                                                           14 YTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV 73
                                                                                                                                                                                                                                                                           14 YRCGESPVWEEASKCLLFVDIPSKTVCRWDSISNRVQRVGVDAPVSSV--ALRQSGGYVA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INC. J. MOI. Med. 5:283-287(2000).
-!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF ENZYMATIC ACTIVITY
IN THE LIVER. DECREASE OF SMP30 LEADS TO THE DYSREGULATION OF
CALCIUM SIGNALING IN THE AGED LIVER.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE SMP-30 / CGRI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||:| : || ||| : ||:|| | : || | | CKLPVDKTTSCCFGGKDYSEMYVTCARDGMSAEGLLRQPDAGNIFKITGLGVKGIA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misawa H., Yamaguchi M.;
"Transcript heterogeneity of the human gene for Ca2+-binding protein
regucalcin.";
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Liver;
MEDLIEE=9604897; PubMed=7548213;
MEDLIEE=9604897; PubMed=7548213;
Eujita T., Mandel J.L., Shirasawa T., Hino O., Shirai T., Maruyama F. Isolation of CDNA clone encoding human homologue of senescence marker protein-30 (SMP30) and its location on the X chromosome.";
Blochim. Blophys. Acta 1263:249-252(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                        23;
                                                                                                                                                                        DB 1; Length 299;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Senescence marker protein-30 (SMP-30) (Regucalcin) (RC).
                                                                                                                       N -> D (IN REF. 1).
E3CF6D3FFCAE4E98 CRC64;
                                                                                                                                                                                      , Pred. No. 6.6e-29;
41; Mismatches 121;
                                                                                                                                                                          Score 454.5;
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                       33389 MW;
                              EMBL; X69021; CAA48786.1; -. EMBL; D38467; BAA07490.1; -. EMBL; D31662; BAA06507.1; -.
                                                                                                                                                                      28.1%;
37.5%;
                                                                                                                                                                                        al Similarity 37.5
111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                       148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; (
Mammalia; Eutheria; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                     PIR; S27203; S27203
                                                                                                                                       299 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=10677570;
                                                                                                   Calcium-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGN OR SMP30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM30_HUMAN
ID SM30_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                   134
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                                                                                                                                       SEQUENCE
                                                                                                                                                                        Query Match
                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                015493;
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                                                                                                                                                                                                                                                                                                                                                     REVVSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDA 129
                                                                                                                                                                                                                                                                                                                                                                          DYDASTLSISNORPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 GLPVGPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEY 184
                                                                                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 GEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKY---TFCKVDKLVSFIIPLAG----SPG
                                                                                                                                                                                                                                                                                                            17 GESPVWEEVSNSLLFVD------PAKKVCRWDSFTKQVQRVTMDAPVSSVALRQSG
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Durovic P.V., Potter S., Dennis P.P.; Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SMP-30 / CGR1 FAMILY.
-!- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A RNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
115-JUL-1998 (Rel. 36, Last annotation update)
Hypothetical 31.5 kba protein.
Sulfolobus acidocaldarius.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                   33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.2%; Score 391.5; DB 1; Length 275; 33.0%; Pred. No. 5.7e-24; ive 51; Mismatches 97; Indels 51;
                                                                                                                                                                                                                 Length 299;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31544 MW; D949D5BF83EBE582 CRC64;
                                                                                                                                                                                     299 AA; 33253 MW; 95BA1C73B7B77635 CRC64;
                                                                                                                                                                                                                                                   42; Mismatches 113;
                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                   27.8%; Score 448.5; DB 36.9%; Pred. No. 2e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 AA
institutions as long
                                                                                                 EMBL; AB028125; BAA78693.1; -. EMBL; AB032064; BAA84082.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U05664; AAA73413.1; -.
                                                                                   EMBL; D31815; BAA06602.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 33.0
Matches 98; Conservative
                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                     Genew; HGNC:9989; RGN.
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275 AA; 3
                                                                                                                                                                                                                                       Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2285;
                                                                                                                                                                     Calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
SEQUENCE 27
                                                                                                                                                     MIM; 300212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y31K_SULAC
P46218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT
                                                                                                                                                                                                                                         Best Local Sim
Matches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sulfolobus
                                                                                                                                                                                     SEQUENCE
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Gaps

51;

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FVVSLEREIAIL----TWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMA 126
                                                                                                                70 YLVKDKDQISLLYEVKDWD-------SRNRFNDGKCDQMGKYWIGTMN 110
                                                                                                                                                                         127 IDAGLPVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDY 186
                                                                                                                                                                                              167 DLERGDISQREVLIDLKEYE--GVPDGMTIDSEGNLWVALYGGGAVLRIDVEKRKVIQE- 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,
Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,
Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
A choi S.K., Codani J.J., Connecton I.F., Cummings N.J., Daniel R.A.,
A choi S.K., Codani J.J., Connecton I.F., Cummings N.J., Daniel R.A.,
Britan K.D., Errington J., Fabret C., Ferrari B., Foulger D.,
A chiseppi G., Guy B.J., Hajer K., Ehrlich S.D., Emmerson P.T.,
A chiseppi G., Guy B.J., Hajer K., Halech J., Grandi G.,
A chiseppi G., Guy B.J., Hajer K., Halech J., Harwood C.R., Henut A.,
Hilbert H., Holsappel S., Rosono S., Hullo M.F., Itaya M., Jones L.,
A turbert H., Holsappel S., Rosono S., Hullo M.F., Itaya M., Jones L.,
A turbert H., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
A kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
A Medina N., Mellado R.P., Mizuno M., Moestl D., Nakal S., Noback M.,
A Noone D., O'Reilly W., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
A Rivolta C., Roche B., Rapoport G., Rey M., Reynolds S.,
A Reger M., Rivolta C., Roche B., Rose M., Sadale Y.,
A Satto T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Satto T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
A Reger M., Tamakoshi A., Tanaka T., Tarpstra P., Tognoni A.,
A Taxeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
A Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vanner T.
                                                                                                                                                                                                                                                                                                                                               247 VKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVY--RVTGLGVKGF 301
                                                                                                                                                                                                                                                                                                                                                                        224 LRLPAPRVTSVIFGGSNMDTLFITTANDHPD-------GGFVYSERVDVKGVETY 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
B
                             EGPIWAY--NSLYFVDIPKGELHN-LKEDGTHWVVKFPTYVSSLQPTKRGGIIVTAGNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The yvsA yvqA (293 degrees - 289 degrees) region of the Bacillus subtilis chromosome containing genes involved in metal ion uptake and
--- LAGSPGR
                                                                                                                                                                                                                                                            187 DASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98304083; PubMed-9639930;
Wipat A., Brignell C.S., Guy J.B., Rose M., Emmerson P.T.,
Harwood C.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
EGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein yvrE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a putative sigma factor.";
Microbiology 144:1593-1600(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YVRE_BACSU 034940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=168;
                                             13
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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zymomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNL_ZYMMO
Q01578;
                                                                                                                                                                12
                                                                                                                                                                                                                                                                      115
                                                                                                            Query Match
                                                                                                                        Local
                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNL_ZYMMO
    SSSSSE 8
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                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | | | | | | | | | :: | AKYSKDELIMTWKDGFYLYHLRDDSLEKIKQPRDMHESLRFNDAKCDPYGRLWAGTTSME 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STLSISNORPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLLDTVK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                    ER----EIAILTWDG---VSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAID 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGLPVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G----EQKQASLYRLNLDGSLVKIKDQVSTSNGLDWDRERNLMYYIDTPTQEIVRYSYDP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCBUSNPEPVIREDQSD--GLPDGMTIDQNGMLMVALFGGSRVVHIDPFQKKE-INSIS 231
                                                                                                                                                                                                                                                                                                                                                                             VGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVVSL 75
                                                                                                                                                                                                                                                                                                                                                                                                          58
                                                                                                                                                                                                                                                                                                                                                                                              Viari A., Wambutt.R., Wedler E., Wedler H., Weitzenegger T., Wifers P., Wipat A., Yamamoto H., Yamamoto K., Yasumoto K., Yashida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                     28;
                                                         Sublins.,
Nature 390:249-256(1997).
Nature 390:249-256(1997).
-! SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE SMP-30 / CGR1 FAMILY.
                                                                                                                                                                                                                                                                                                                        ; Score 376; DB 1; Length 292; Pred. No. 1e-22; 52; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                   le-22;
~hes 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-JCM 9061;
Cho T., Sudoh M., Tanaka T., Nakashima Y.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN THE CELL GROWTH REGULATION.
                                                                                                                                                                                                                                                                                  n; Complete proteome.
33204 MW; D68A0812FC8D90AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCILUM: INVOLVE ... SIMILARITY: BELONGS TO THE SMP-30 / CGRI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 IPDPQVTSVAFGGPNLDELHVTSAGLQLDD 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ223978; CAA11732.1; -.
                                                                                                                                                                                                                                                                                                                         23.3%;
31.5%;
                                                                                                                                                                                                                                          EMBL; Z99120; CAB15310.1; -. EMBL; Z99121; CAB15325.1; -.
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 31.5
Matches 85; Conservative
                                                                                                                                                                                                                                                                    SubtiList; BG14145; yvrE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell growth protein CGR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Candida albicans (Yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                al protein;
292 AA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998
15-JUL-1998
15-JUL-1998
                                                                                                                                                                                                                                                                                  Hypothetical
SEQUENCE 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGR1_CANAL P56553;
                                                                                                                                                                                                                                                                                                                                                                                                                                    92
                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
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CGR1_CANAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 -IPLAGSPGRFVVSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNN-----RLNDGKA 114
                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: D-glucono-1,5-lactone + H(2)0 = D-gluconate.
-!- PATHWAY: SECOND STEP IN SORBITOL PATHWAY.
-!- SUBUNIT: HOMODIMER.
-!- SUBCELLULAR LOCATION: Periplasmic (Probable).
-!- CAUTION: IT IS POSSIBLE THAT IN SOME CASES MET-40 IS THE INITIATOR IN THIS CASE THE EXPRESSED ENZYME WOULD REMAIN CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochim. Biophys. Acta 1171:198-200(1992).
-!- FUNCTION: HYDROLYZES THE GLUCONOLACTONE FORMED BY GLUCOSE-FRUCTOSE OXIDOREDUCTASE, AND THAT FORMED IN AEROBIC CONDITIONS BY THE
                                                                                                                                                                                                                                                                                                                                                                                            GKYTVGEGPHWDHETQTLYFVDTVEKTFHKYV------PSQKKYTFCKVDKLVSFI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPLGNLWTGTMAIDAGLPVG-----PVTGSLYHLGADKKVK------MHESNIAIANGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 DPWGNLWIGVM----NDFPIGAKEGIQPEGKLYRIGFSKESNKLTCDVMIENSL-ISNGLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 GNLWVAVFQGQRIIKISTQQPEVLLDTVKIPDPQVTSVAFG-GPNLDELHVTSAGLQLDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 WSNDLKKMYYIDSGKRRVDEYDYDASTLSISNQRPLFTFEKHEVP----GYPDGQTIDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kanagasundaram V., Scopes R.;
"Isolation and characterization of the gene encoding gluconolactonase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Gluconolactonase precursor (EC 3.1.1.17) (D-glucono-delta-lactone
                                                                                                                                                                                                                                                                                                                           50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zymomonas mobilis.
Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
                                                                                                                                                                                                                                                              Length 340;
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                            EMBL; AB013716; BAA28176.1; -.
SEQUENCE 340 AA; 38391 MW; 4B1673ED448D1F7A CRC64;
                                                                                                                                                                                                                                                           14.6%; Score 235; DB 1; Le 26.9%; Pred. No. 1.9e-11; ive 55; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 AA
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STRAIN-ATCC 29191 / ZM6;
MEDLINE-93129619; PubMed-1482681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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302 EKATIDATNLDG 313
                                                                                                                                                                                                                                                                                                                           84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279 --SSLDKSLVNG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from Zymomonas mobilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1993 (Rel. 26, 01-JUL-1993 (Rel. 26, 01-OCT-1993 (Rel. 27,
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us-10-089-986-2.rsp

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52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
PIR; S45911; S45911.
SGD; S0000257; YBR053C.
                            Hypothetical protein. SEQUENCE 358 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR005225;
                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlorella vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                             EFTU_CHLVU
                                                                                                                                                                                                                                                                     213
                                                                              Query Match
Best Local
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                78 EIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLW---TGTMAIDAGLPVG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 PVTRQRSVVDNYKGKRENSPNDLFFSKSGAVYFTDPPYGLTNLDESDIKEMNYNGVFRLS 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 EGPVWVKNGNFLLFSDPPANIMRKWTP------DAGVSIFLKPSGHAEPIPAGOFR 125
                                                                                                                                                                                                                                                                                                                                                                                                                               135 PVT-------HLG 144
                                                                                                                                                                                                                                                                                                      EGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVVSLER
                                                                                                                                                                                                                                                                                                                                                                                                 126 E-----PGS-----MKVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 ADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLSISNQRPLF-TFE
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aljinovic G., Pohl T.M.; ^{\circ} Sequence and analysis of 24 kb on chromosome II of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota: Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                        66
                                                                                                                                                                                                                                       7.7%; Score 124.5; DB 1; Length 320; 21.8%; Pred. No. 0.0099; tive 26; Mismatches 83; Indels 99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-007-1994 (Rel. 30, Created)
01-007-1994 (Rel. 30, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Hypothetical 40.3 kDa protein in REG2-YRO2 intergenic region.
YBR053C OR YBR0506.
                                                                                                                                                                                           (MINOR FORM).
                                                                                                                                                                                          GLUCONOLACTONASE (MINOR FOR 7552DE348D83564C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cerevisiae.";
Yeast 11:475-479(1995).
-!- SIMILARITY: BELONGS TO THE SMP-30 / CGR1 FAMILY.
                                                        EMBL, X67189; CAA47637.1; -.
PIR; S25124; S25124.
PIR; S28218; S28218.
InterPro; IPR000033; Ldl_receptor_rep.
SMART; SM00135; LY; 1.
Hydrodase; Serine estrase; Periplasmic; Signal.
SIGNAL
                                                                                                                                                                            GLUCONOLACTONASE.
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    not removed.
   modified and this statement is not removentities requires a license agreement (Soor send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95321020; PubMed-7597852;
                                                                                                                                                                                                          320 AA; 34767 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 235922; CAA84996.1; -. EMBL; 246260; CAA86396.1; -.
                                                                                                                                                                                                                                                           Similarity 21.89 S8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YBQ3_YEAST
P38235;
                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                         18
                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                        148 RSNDGNVSPDGKYIYVGLMS-DFPFDLEPI-GCLLRVDLLAHKIELVWNCLLIPNAIHWD 205
                                                                                                                                                                                                                                                                                                                                              206 ESDQKTMYVTDSLNFTIWKCPGGDLLKRDELIDVKNS----NNQ----SFESPE----PD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 RLNDGKADPLGN-LWTGTMAIDAGLPVGPVTGSLYHLG-ADKKVKMHESNIAIANGLAW- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                   GQTI-----DEEGNLWVAVFQGQRIIKISTQQPEVLLDTVKIPD--PQVTSVAFGGPNL 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales; Chlorellaceae; Chlorella.
                                                                                                                                                                                                                                                                                                             165 SNDLKKMYYIDSGK-----RRVDEYDYDASTLSISNQRPLFTFEKHEVPGYPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBCELLULAR LOCATION: Chloroplast.
-i- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S., Tsudzuki J., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta Inamura A., Yoshinaga K., Sugiura M., Sugitura M., Complete nucleotide sequence of the chloroplast genome from the green alga Chlorella vulgaris: the existence of genes possibly involved in chloroplast division."; Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).

-I. FUNCTION: THIS PROPEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROFEIN
                                                                                                                      46;
                                                           Length 358;
                                                                                                                      73; Indels
0091701F98ED87C9
                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 KDLFVTTANAEINDAVRTNTDKN--GGCIYKI 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 DELHVTSAGLQLDD---SSLDKSLVNGHVYRV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409 AA
                                                                                           ; Pred. No. 1;
41; Mismatches
                                                              Score 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=IAM C-27 / Tamiya;
MEDLINE=97303241; PubMed=9159184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFTU_Cterm.
EFTU_D2.
EF_GTPbind.
Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB001684; BAA57886.1; -. HSSP; P07157; 1AIP.
   40295 MW;
                                                           6.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004541; EF-Tu.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 HL-----DEKVDDFLLGGI-AGTVPAAAGHPVGYDIDDANLYDEOWEANSEKIESMLED 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIKNNRLNDGKADP--LGNLWTGTMAIDAGLPVG-----PVTGSLYHLGADKKVKM--- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----PIIRESEAVFGEGR--AGMFEDERFSVGTAGVLEAIADT-----DCFSVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GP-VVEKIAELGKYTV------GEGPHWDHETQT-LYFVDTVEKTFHKYVPSQKKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 TFCKVDKLVSFIIPLAGSPGRFVVSLERE----IAILTWDG---VSAAPTSIEAIVNVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HESNIAIANGLAWSN-------DLKKMYYIDSGKRRVDEYDYDASTLSISNQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 HRDQITLAVDLAYEDENDDRAEQAVDDIDEKRLSYLDVGSETLMEYS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLLDTVKIPDPQVTSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last unoctation update)
Protocadherin Fat 2 precursor (Multiple epidermal growth factor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 FGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKG-----FAGVKV 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGD-----TSRAIEMYGMEEDEF---GHVSIAGGAYIRALTRAQLVGVEV 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.8%; Score 94; DB 1; Length 401; 22.1%; Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137; Indels
                                                                                                                                                                                                                                                                                                                                                     ACDD98F8856B490E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4351 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Mismatches
                                                                                                                                                                                                                                Pfam; PF00162; PGK; 1.
PRINTS; PR00477; PHGLYCKINASE.
PROSITE; PS00111; PGLYCERATE_KINASE; 1.
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                                                                                                                                                                                                                                                                                                                          Transferase, Kinase, Glycolysis.
SEQUENCE 401 AA; 44193 MW; AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                               EMBL; L47295; AAB03731.1; -. HSSP; P18912; 1PHP.
                                                                                                                                                                                                        InterPro; IPR001576; PGK.
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                                                                                                                                                                                                                                                                                                                                                     401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
tes 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
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FAT2 OR MEGF1.
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Matches
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European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 LEREIAILTWDGVSAAPTSIEAIVNVE-PHIKNNRLN------DGKADPLGNLWTGTM 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 QMDGGILVVSGADGPMPQTKEHLLLAKQV-----GVPNIVVFLN------K 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 EDOVD-DAELLELLELEIRETLDKYEFPG-----DE----IPIISGSALLALEALTE 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----GPNL-----DELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFAGVKVK 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 TIG---HVDHGKTTLTAAITMA-------LAARGGAKGR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 -----KYDDIDSAPEEKARGITINTAHVEYETENRHYAHVDCPGHADYVKNMITGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 TVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 VDEYDYDASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKIS--TQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ø
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"Higher-plant chloroplast and cytosolic 3-phosphoglycerate kinases: case of endosymbiotic gene replacement.";
Plant Mol. Biol. 30:65-75(1996).
-!- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-phospho-D-glyceroyl phosphate.
-!- PATHWAY: Second phase of glycolysis; second step.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 141;
                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 409;
                                                                                                                                                                                                                                                           GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
0183143E5E117999 CRC64;
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                                                                                                                                                                       PROSITE; PS00301; EFACTOR GTP; 1.
Elongation factor; Protein biosynthesis; Chloroplast;
GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phosphoglycerate kinase (EC 2.7.2.3).
                                                                                                                                                                                                                                                                                                                                                                                                       5.9%; Score 94.5; Di 19.6%; Pred. No. 3.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ed. No. 3.2;
Mismatches
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
PRINTS; PR001315; ELONGATNECT.
TIGRPAMS; TIGR00231; Small_GTP; 1.
TIGRFAMS; TIGR00485; EF-TU; 1.
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                                                                                                                                                                                                                                                                                                                    136 139 G'
409 AA; 44911 MW;
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(Rel. 34, Last seq
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Halobacteriaceae; Haloarcula.
NCBI_TaxID=28442;
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                                                                                                                                                                                                                                                              26
85
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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81
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P50315:
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SEQUENCE
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           Euteleostomi;
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                                                                                                                         TISSUE=Brain;
MEDLINE-98360089; PubMed=9693030;
MRAyamam M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O Makayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara C Edentification of high-molecular-weight proteins with multiple EGF-like motifs by motif-trap screening.";
Genomics 51:27-34(1998).
                                                      MEDLINE-20202559; PubMed-10716726; Wu Q., Maniatis T.; "Large axons encoding multiple ectodomains are a characteristic feature of protocodherin genes."; Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
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                                                                                                                                                                                                            POUSTEA A., Weil B., Wiemann Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 32 CADHERIN DOMAINS.
-!- SIMILARITY: CONTAINS 1 LAMININ G-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
           Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CADHERIN 2.
CADHERIN 3.
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CADHERIN 6.
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CADHERIN 8.
CADHERIN 9.
CADHERIN 10.
CADHERIN 10.
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SWART; SW00112; CA; 32.
SWART; SW00118; EGF; 2.
SWART; SW00282; LamG; 1.
PROSITE; PS00232; CADHERIN_1; 14.
PROSITE; PS50268; CADHERIN_2; 32.
PROSITE; PS00022; EGF_1; 2.
PROSITE; PS01186; EGF_1; 1.
PROSITE; PS50025; LAM_G_DOMAIN; 1.
Transmembrane; Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                EMBL; AF231022; AAF61928.1; --
EMBL; AB011535; BAA33463.1; --
EMBL; ALS7443; CAB75663.1; --
Genew; HGNC:3596; FAT2.
MIM; 604269; --
INTESP; PO0740; IEDM.
InterPro; IPR001216; Cadherin.
InterPro; IPR001791; Laminin_G.
Pfam; PF000028; cadherin; 33.
Pfam; PF000028; cadherin; 33.
Pfam; PF00008; EGF. 2.
PRINTS; PR00205; CADHERIN.
                                                                                                       [2]
SEQUENCE OF 3777-4349 FROM N.A.
                                                                                                                                                                                   [3]
SEQUENCE OF 4142-4349 FROM N.A.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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1.1e+02;
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6C050CA17AD398ED CRC64;
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EGF-LIKE 2.
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CADHERIN 31.
CADHERIN 32.
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Best Local Similarity 21.9
Matches 80; Conservative
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                                                                          2840 PGSNVHEL-FAIDSESGWITTLQEL------DCETCQ-----TYHFH- 2874
                                                                                                                                                                                                                                                                                                              2875 VVAYDHGQTIQLSSQALVQVSITDENDNAPRFASEEYRGSVVENSEPGELVATLKTLDAD 2934
2935 ISEQNRQVICYITEGDPLGQFGISQVGDEWRISSRKTLDREHTAKYLLRVTASDGKFQAS 2994
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                                                                                                                              --GSL-YHLGAD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-96257210; PubMed-8675024; Ratayama M., Sakai Y., Okamoto S., Ihara F., Nihira T., Yamada Y.; Katayama M., Sakai Y., Okamoto S., Ihara F., Nihira T., Yamada Y.; "Gene organization in the ada-rplL region of Streptomyces virginiae."; Gene 171:135-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOWAL RNA AND IS LOCATED IN THE BEIGHBORHOOD OF THE SITE WHERE ELONGATION FACTOR TU IS BOUND TO THE RIBOSOME (BY SINILARITY).
SIMILARITY: BELONGS TO THE LIP FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                      147 KKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLSISNQRPLFTFEXHE
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                    DKLVSFIIPLAGSPGRFVVSLEREIAIL----TWDGVSAAPTSIEAIVN---
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Last annotation update)
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Pfam; PF00687; Ribosomal_L1; 1.
ProDom; PD001314; Ribosomal_L1; 1.
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Matches 41; Conservative
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Gaps

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ETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVVSLEREIAILTW
                                                                                                                                         120 LWTGTMAIDAGLPVGPVTGSLYHLGADKKVKMH 152
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Search completed: August 1, 2003, 14:32:45 Job time: 27 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries

    protein search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

sp_bacteriap:*

sp_archeap:* sp_rvirus:*

sp_vertebrate:*

sp_plant:*
sp_rodent:*
sp_rident:*

sp_fungi:*
sp_human:*
sp_invertebrate:*

sp_organelle:* sp_phage:*

sp_mammal:* sp_mhc:*

Score 81515 81615 81615 859.5 859.5 851 821 821 8474.5 8453.5 8453.5	SUMMARIES	Query Match Length DB ID Description	308 5 Q95YI4 Q95yi4	55.1 309 5 Q8TA67 O8ta67 luciola cru	307 5 Q8TA68 08ta68	303 S Q9NDS6	303 5 Q9VFG5	303 5 Q9VYR1	306 5 09NDP1	306 5 Q9BID6	299 13 091922	299 13 Q9IBA8	299 13 091923	299 11 Q925W3	267 5 Q95PD9		C 1100 Vr 101
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Result No. 1 1 1 2 8 8 3 8 5 8 5 6 6 6 7 9 10 4 7 11 1 4 7 1 1 1 1 1 1 1 1 1 1 1 1 1		Score	1615	889.5	859.5	1 568	5 568	5 550	538	521	474.5	470.5	455	453.5	3 445.5	423.5	

Dp $^{\circ}$ QQ õ qq

17	ated) t sequence update) t sequence update) t annotation update) n firefly). Tracheata; Hexapoda; Insecta; ota; Coleoptera; Polyphaga; mpyridae; Photinus. Luciferin."; 2001). 4403A6EC6459A378 CRC64; core 1615; DB 5; Length 308; red. No. 1.8e-125; Mismatches 0; Indels 0; Gaps	MGPVVEKIAELGKYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSF 60
2882 2882 2882 2883 2883 3883 3883 3883	(TrEMBLrel. 1 (TrEMBLrel. 1) (TrEMBLrel. 1) (TrEMBLrel. 1) Generating er alis (North Petazooa; Arth ectazoa; Arth ectazoa; Arth ectazoa; Pubmeda; Salos, Pubmeda; Eantharoic 054; Lantharoic no a Luminescy no a Regenerate	IAELGKYTV IAELGKYTV
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17 365.5 18 350.5 20 348 21 331.5 22 348.5 24 29.5 27 288.5 28 29.5 29 29.5 20 29.5 21 331.5 22 29.5 23 31.5 24 20.5 26 20.5 37 20.5 38 20.5 39 20.5 30 20.5 31 20.5 32 20.5 33 20.5 34 20.5 36 20.5 37 20.5 38 20.5 39 20.5 30 20.5 31 20.5 32 20.5 33 20.5 34 20.5 36 20.5 37 20.5 38 20.5 39 20.5 30 20.5 30 20.5 31 20.5 32 20.5 33 20.5 34 20.5 36 20.5 37 20.5 38 20.5 39 20.5 30 20.5	1 1 295X14 295X14; 201-DEC-20 201	u u
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08TA67; Q8TA67 RESULT 2 Q8TA67

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WIGTMAIDAGL-PVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 PEVLLDTVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGPVVEKIAELGKYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Senescence marker protein-30 (SMP-30).

SMP-30 OR CG7390.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Petryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Expression of Drosophila homologue of senescence marker protein-30 during cold acclimation.";
                                                                                                                                                enzyme
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                                                                                                                                                                                                                                                 307;
                                                                                                             SEQUENCE FROM N.A. Gajiyama N.; Gomi K., Hirokawa K., Kajiyama N.; Gomi K., Hirokawa K., Kajiyama N.; Inciterin-regenerating (LRE) cDNA in Luciola cruciata and Luciola lateralis."; Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AB07247; BAB85478.1: BODIENCE 307 AA; 34286 MW; B03CED0AC609A92C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.2%; Score 568; DB 5; Length 30
40.7%; Pred. No. 6.9e-39;
iive 48; Mismatches 116; Indels
                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inser
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga
Elateriformia; Cantharoidea; Lampyridae; Luciola
                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                 Indels
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                               85;
                                                                                                                                                                                                                                              53.2%; Score 859.5; DB 5
52.8%; Pred. No. 5.5e-63;
ive 58; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303
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EMBL, AB020490; BAA92938.1; -
Flybase, FB900039257; smp-30.
SEQUENCE 303 AA; 33349 MW; 68F12B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-CANTON S; TISSUE-WHOLE BODY;
PubMed=10817837;
Goto S.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2001 (TrEMBLrel. 16,
              Luciola lateralis (Firefly).
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                                                                                                                                                                                                                                                                   Local Similarity 52.8
nes 163; Conservative
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                                                                                 NCBI_TaxID=7052
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Best Local $
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 QQPEVLLDTVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLG
               VDEYDYDASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Gomi K., Hirokawa K., Kajiyama N.;

Gomi K., Hirokawa K., Kajiyama N.;

Modecular cloning and expression of luciferin-regenerating enzyme (LRE) cDNA in Luciola cruciata and Luciola lateralis.";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB072448; BABB5479.1;

SEQUENCE 309 AA; 33804 MW; BE33C4E2IEF5IE6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
                                                                                                                                                                                                                                                                                                                                                                     Luciola cruciata (Japanese firefly) (Genji firefly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Elateriformia; Cantharoidea; Lampyridae; Luciola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.1%; Score 889.5; DB 5; Length 309; 56.6%; Pred. No. 1.8e-65; ive 47; Mismatches 83; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   087A68;
01-JUN-2002 (TrEMBLrel. 21, Created) .
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Luciferin-regenerating enzyme.
                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Luciferin-regenerating enzyme.
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VKGLPGDRVKL 309
                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                      FAGVKVKL 308
                                                                                                                                                       FAGVKVKL 308
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Query Match

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REC STRAIN-BERKELEY,

RA Adding N. A.

RA Adding M. N. A.

RA Adding M. D. Celniker S.E., Holf R. A., Evans C.A., Gocayne J.D.,

RA Adding M. D. Celniker S.E., Holf R. A., Hoskins R. A., Galle R. E.,

RA Adding M. D. Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA Brandon R.C., Rogers Y. H.C., Blazel R.G., Champe M., Pfelifer B.D.,

RA Brandon R.C., Rogers Y. H.C., Blazel R.G., Champe M., Pfelifer B.D.,

RA Abril J.F., Appayani A., An H. J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Appayani A., An H. J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Appayani A., Barman B.P., Bhandari D., Bolshakov S.,

RA Abril J.F., Appayani A., Barman B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Gabriellan A.E., Garys A.D., Dew I., Dietz S.M.,

RA Clordy J.M., Cawley S., Dahlke C., Perriers S., Fleischmann W.,

RA Clodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houston K.A., Howland T.J., Helman T.J., Hernandez J. Moshrefi A.,

RA Harris N.L., Haush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Harris N.L., Haush P., Karpen G.H., Ke Z., Kennison J.A., Mattei B.B., McIntoch T.C., McHeod M.P., McPherson D.,

RA Mantel B.E., McIntosh T.C., McHeod M.P., McPherson D.,

RA Malson D.R., Holson R., Naxon K., Naxiers R., Pacleb J.M.,

RA Harris N. P., Patland S., Pollard J., Pull Y., Rese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Spier E., Spradling A.C., Stapeleton M., Strong R., Snith T.,

RA Spier E., Spradling A.C., Stapeleton M., Strong R., Williams S.M., Woodage T., Weilley Williams S.M., 
                                                                                          SNQRPLFTFEK--HEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLLDTVKIPD 251
                                                                                                                                                                                                                                                                   PQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFAGVKVKL 308
                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                            134 GPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLSI
                                                                          SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV
             VGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDK--LVSFIIPLAGSPGRFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbaun J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CG7390 protein (RE17477p).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7227;
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74 SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 VGEGPHWDHETQTLYFVDIVEKTFHKYVPSQKKYTFCKVDK--LVSFIIPLAGSPGRFVV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 PQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFAGVKVKL 308
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (Regucalcin HOWOLOGUE).
REGUCALCIN OR CG1803.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Ephygota; Mooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephygotodae; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                        Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBqn0038257; smp-30.
SEQUENCE 303 AA; 33377 MW; 68F92692E1AC88AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.2%; Score 568; DB 5; Le
40.7%; Pred. No. 6.9e-39;
iive 48; Mismatches 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003706; AAF55095.1; -. EMBL; AY071130; AAL48752.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 40.73
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     STRAIN-BERKELEY;
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118
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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra de Pablos B., Delcher A., Deng Z., Mays A.D., Dow I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Rasler E., Garrell J.H., Gu Z., Guan P., Harris M., Glasser K., RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Kaler C., Kravitz S., Kulp D., Lai Z., Alalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Mimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Rattei B., McIntosh T.C., McLeod M.P., McDherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Merkulov G., Milshina N.V., Mobarry C., Steeler F., Shen H., RA Palazzolo M., Pittman G.S., Panner S., Pollard J., Puri V., Resse M.G., RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Spier E., Shen G., Steeleton M., Strong R., Sun E., Stradling A.C., Stapleton M., Strong R., Sun E., Sheng X.H., Woodage T., Worls K., Wu D., Yang S., Yao, Q.A., RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao, S., Zhan X., Zhang S., Zhan X., Zhang S., Zhan X., Zhang S., Zhan X., Zhu S., Zhan X., Zheng X.H., Wang S., Zhan X., Zhos R., Myers E.W., Rubin G.M., Venter J.C., Staplere E.W., Rubin G.M., Venter J.C., Stablere E.W., Rubin G.M., Venter E.W., Smith H.O., Rubin G.M., Venter E.W., Smith H.O., Rubin G.M., Wenter E.W., Smith H.O., Rubin G.M., Rubin G.M., Rubin G.M., Rubin G.M., Rubin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 TLSISNQRPLFTFEKHEVPGY--PDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLLDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 KIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFAGVKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 LGEGPHWDVARQSLYYVDLEAGSLLRYDYAQNKVYKTKIEGETLAGFVLPVEGRPQEFAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F9AD6EB15E758209 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 550; DB 5;
Pred. No. 2.1e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20250851; Pubmed-10788801; Nakajima Y., Natori S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003487; AAF48129.1; -.
EMBL; AB036904; BAA99283.1; -.
Flybase; FB900030362; regucalcin.
SEQUENCE 303 AA; 33644 MW; F9
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118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Best Local S
Matches 118
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Q9NDP1
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PRT;

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TISSUB-ANTERIOR FAT BODY;
Hansen I.A., Meyer S.R., Schaefer I., Scheller K.;
Hansen I.A., Meyer S.R., Schaefer I., Scheller K.;
Identification of the anterior fat body protein as interactor of the hexamerin receptor in the blowfly Calliphora vicina.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY028616; AAK26774.1;
SEQUENCE 306 As; 34289 MW; 497241A2424C2C19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 IIPLAGSPGREVVSLEREIAILTWDGVSAAPTSIEAIVNV---EPHIKNNRLNDGKADPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 KRRVDEYDYDASTLSISNQRPLFTFEKHEVPGY--PDGQTIDEEGNLWVAVFQGQRIIKI
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24] NPTTGKVLLE-IKFPCKQITSAAFGGPNLDILYVTTS-----SRFGEPDPAGTTYKVTG
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Anterior fat body protein.
Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphora.
                                                                                                                                                                         Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).
Bukaryota; Metazoa; Arthropoda Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroldea; Sarcophagidae; Sarcophaga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 PVVEKIAELGKYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKV:--DKLVSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNLWTGTMAIDAGLPVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakajima Y., Natori S.; "Identification and characterization of an anterior fat body protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Blochem. 127:901-908(2000).
EMBL, AB036903; BAA99282.1; -.
SEQUENCE 306 AA; 34319 MW; 77CFF54575D7E8E7 CRC64;
                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.3%; Score 538; DB 5; 39.0%; Pred. No. 2.1e-36;
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    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-FAT BODY;
MEDLINE-20250851; Pubmed-10788801;
(TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 16,
                                                                                                                                       Anterior fat body protein.
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294 LGAKGYPMTKIQL 306
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Best Local Similarity 39.0'
Matches 122; Conservative
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134 GPVT-----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDA 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 RPAVVERNOGSLFTLYPDHSVVKHFDMVDISNGLDWSLDHKTLYYIDSLSFKVDALDYDM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 YTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 STLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
   247 VKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 VKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                          Eukaryotā; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mphibla; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBL_TaxID=8355;
                                                                                                                                                                                                                                                                                                                             MEDLINE=20193502; PubMed=10727865; Sato A., Asashima M., Yokota T., Nishinakamura R.; Specific Medh. Dev. 92:273-275(2000).

EMBL; AB033368; BAA93719.1; SEQUENCE 299 AA; 33073 MW; BABB9749258BB41C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.1%; Score 470.5; DB 13; Length 36.8%; Pred. No. 7.9e-31; ive 47; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                        299 AA
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                                                                                                                                                                                                               Xenopus laevis (African clawed frog).
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                                                                                                        PRT;
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                                                                                                                                                                                Senescence marker protein-30.
XSMP-30.
                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misawa H., Yamaguchi M.;
                                                                                                        PRELIMINARY;
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Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109; Conserva
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. TISSUE-ANIMAL CAP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=LIVER;
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Best Local
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                                                                          RESULT 10
Q9IBA8
ID Q9IBA
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                                                                                                                                                                                                 178 KRRVDEYDYDASTLSISNQRPLFTFEKHEVPGY--PDGQTIDEEGNLWVAVFQGQRIIKI 235
                                                                                                                                                                                                                                                                                                 STQQPEVLLDTVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTG 295
                                                                                                                                                                                                                                                                                                                  241 NPTTGQVLE-IKFPCKQITSAAFGGPNFHILFVTTS-----SRFGEPHPAGTTXKVTG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IIPLAGSPGRFVVSLEREIAILTWDGVSAAPTSIEAIVNV---EPHIKNNRLNDGKADPL 117
                                                                                                                                                62 AVPVEGTTDQFAVGSGRRVVIVQWDGVSETAKVLKTLFEVQTGDERFTGNRFNDGKCDPR 121
                                                                                                                                                                              GNLWTGTMAIDAGLPVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSG 177
                                                                         3 PVVEKIAELGKYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKV--DKLVSF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 YTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STLSISNQRPLFTFEXHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLDT
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                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misawa H., Yamaguchi M.; "The gene of Ca2+-binding protein regucalcin is highly conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 29.4%; Score 474.5; DB 13; Length 299; Best Local Similarity 37.2%; Pred. No. 3.7e-31; Matches 110; Conservative 46; Mismatches 117; Indels 23;
 Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vertebrate species.";
Int. J. Mol. Med. 6:191-196(2000).
EMBL; AB037936; BAA90694.1; -
SEQUENCE 299 AA; 33087 MW; BABB9749258BB2C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01922;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 Score 521; DB 5;
Pred. No. 5.4e-35;
4; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20351777; PubMed=10891565;
                             44;
32.3%;
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LGAKGYPMTKIQL 306
                                                                                                                                                                                                                                                                                                                                                              LGVKGFAGVKVKL 308
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=LIVER
                             122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Regucalcin.
                                                                                                                                                                              118
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   Query Match
                  Local
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                             Matches
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GKADPLGNLWTGTMAIDAGLPVGPVTGSLYHLGADKKVKMHESNIALANGLAWSNDLKKM 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 YYIDSGKRRVDEYDYDASTLSISNQRPLFTFEKHEVPGY--PDGQTIDEEGNLWVAVFQG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 QRIIKISTQQPEVLLDTVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGH 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDLAGFAVPVEGTIDQFAVGSGRRVVIVQWDGVSETAKVLKTLFEVQTGDERFIGNRFND 76
183 PTGQISNRRTVYKMEKDE--QIPDGMCIDVEGKLWVACYNGGRVIRL---DPETGKRLQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 DKLVSFIIPLAGSPGRFVVSLEREIAILTWDGVSAAPTSIEAIVNV---EPHIKNNRLND
                                                                                                                                                                                                                                                                                                                                                                                                                                            calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
Eukaryota; Metazoa; Arthropoda: Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ocetroidea; Calliphoridae; Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IISSUE=FAT BODY;
Hansen I.A., Meyer S.R., Berlinger M.J., Scheller K.;
"Identification of new interactors of the hexamerin receptor in the
                                                          247 VKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA
                                                                                       01-BEC-2001 (TrEMBLrell. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative calcium binding transcriptional regulatory protein.
RA0381 OR SMA0717.
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid bSymA (megaplasmid 1).
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5; Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              blowily Calliphora vicina.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF326959; AAK51353.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76F4EEA957D032FF CRC64;
                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.6%; Score 445.5; DB 5;
39.4%; Pred. No. 7.8e-29;
tive 37; Mismatches 107;
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                                                                                                                                                                                                                                                       267
                                                                                                                                                                                                                                                                                 095PD9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
Anterior fat body protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 VYRVIGLGVKGFAGVKVKL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 AA; 29836 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccn . 27.0%
al Similarity 39.4%
102; Conservative
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Q92ZR8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LQTGKIGNRRSVYKLEKEE--SIPDGMCIDTEGKLWVACYDGGRVIRL---DPETGKRIQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 TVKLPVDKTTSCCFGGKDXSEMYVTSASDGMDREWLSRQPQAGGVFKITGLGVKGIPPYP 296
                                                                                                                                                                                                                                                                                                                                                                                                   73 VSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                   VGPVT-----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYD 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASTLSISNORPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLD 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKG---- 300
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                                                                                                                                                                                                                                                                                                                          189 STLSISNQRPLETFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 YTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 YRCGESPVWEEASKCLLFVDIPSKTVCRWDSISNRVQRVGVDAPVSSV--ALROSGGYVA
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                                                                                                                                                                                                                                                                                          13 KYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFV
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"The gene family encoding the calcium-binding protein regucalcin.";
"The gene family encoding the EMBL/GenBank/DDBJ databases.
EMBL; AB037934: BAA90692.1; -- SEQUENCE 299 AA; 33390 WW; 5D8F2D95FCA4EE35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
              conserved
                                                                                                                                                                                                                                   28;
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                                                                                                                                                                              Length 299;
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              "The gene of vertebrate species."; vertebrate species."; vertebrate species."; lnt. J. Mol. Med. 6:191-196(2000).
EMBL; AB037935; BAA90693.1; -. FA4C7571164720E CRC64; manner 299 AA; 33229 MW; 4754C7571164720E CRC64; manner 299 AA; 33229 MW; 4754C7571164720E CRC64;
        "The gene of Ca2+-binding protein regucalcin is highly
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Last sequence update)
Last annotation update)
                                                                                                                                                                           28.2%; Score 455; DB 13; 37.0%; Pred. No. 1.5e-29; ive 40; Mismatches 123;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-DEC-2001 (TEMBLEEL: 19,
01-DEC-2001 (TEMBLEEL: 19,
01-DEC-2001 (TEMBLEEL: 19,
                                                                                                                                                                                                                                      Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YDYDASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVL 243
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                                                                                                                                                                                                                                                                                                                                    343 NEGLIVASQDGVEHFDFDRGDFNPFAEP-----EPGLPENRLNDAKVDPSGRLWYG
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SMRLDVSRP----TGSLYRLTSAGEVTRAGSGFTVANGLAWSPDSSTFYFVDTVPGIIYA
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                                                                                                                                                                                                                                                                                                                                                                                76 EREIAILTWDGVS------AAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTG
                          Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Per Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
Sinorhizoblum meliloti psymA megaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
EMBL; AE007229; AAK65039.1;
Enterpro; IPR000289; HTH_ICIR.
Plasmid; Hypothetical protein; Complete proteome.
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                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LD-TVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVY 291
                                                                                                                                                                                                                                                      DB 16; Length 569;
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                                                                                                                                                                                                       al protein; Complete proteome.
60943 MW; EB34C90D654EE8AD CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Transcriptional regulator, IclR family/regucalcin.
ATU5464 OR AGR_PAT_685.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
                                                                                                                                                                                                                                                 26.2%; Score 423.5; DB 16; 34.6%; Pred. No. 1.6e-26; Live 46; Mismatches 102;
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STRAIN=1021;
MEDLINE=21396509; PubMed=11481432;
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Matches 100; Conservative
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NCBI_TaxID=176299;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goodner B., Hinkie G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Heumiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Woughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Gelome sequence of the plant pathogen and biotechnology agent Agrobacterium tunefaciens C58.";

Agrobacterium tunefaciens C58.";

Science 294:233-2338(2001).

EMBL: AB008967; AAL46151.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 VGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVVSL
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                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                             25.4%; Score 409.5; DB 1
33.1%; Pred. No. 2.4e-25;
ive 57; Mismatches 110
MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                 Plasmid; Complete proteome.
SEQUENCE 584 AA; 62034 M
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Best Local Similarity 33.1%
Matches 99; Conservative
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US-09-134-001C-5111

Sequence 5111, Application US/09134001C

Patent No. 6380370

GENERATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOCC
                                                                                                                                                                                                                                                                                                                                                                                          AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 SPGRFVVSLEREIAIL-----TWDGVSAAPTSIEAIVNVEPHIKNNR-LNDGKADPLGN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPAAIKVHKDGRLFICYLGDFKTTGGIFATTEKGEQIEEIISDLNTEYCIDDMVFDSKGG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 LWTGTMAIDAGLPVGPVTGSLYHLGAD-KKVKMHESNIAIANGLAWSNDLKKMYYIDSGK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 RRVDE--YDYDASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRII 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 NRLHRIALEDDGVTIAPFGATIPYYFTGHE---GPDSCCIDSNDNLYVAMYGOGRVL 262
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           US-08-747-221B-14

US-09-005-051-14

US-08-747-221B-58

US-08-747-221B-58

US-09-342-648-2

US-09-887-534A-45

US-09-134-001C-4705

US-09-134-001C-4705

US-09-1489-506-1

US-09-489-506-1

US-08-747-221B-53

US-08-747-221B-19

US-09-005-051-19

US-09-393-6278-1

US-09-393-6278-1

US-09-393-6278-1
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Pred. No. 0.00084;
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: WOLELIC ACID AND AMINO AC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOST;
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
SEQ ID NO 4646
                                                                                                                                                                                                                                                                                                                                    Sequence 4646, Application US/09134001C Patent No. 6380370
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Similarity
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Sequence 6, Appli
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Sequence 2, Appli
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                                                                                    August 1, 2003, 14:32:13 ; Search time 24 Seconds (without alignments) 377.594 Million cell updates/sec
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                                                                                                                                                                     1 MGPVVEKIAELGKYTVGEGP......HVYRVTGLGVKGFAGVKVKL
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Compugen Ltd
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US-09-397-885-3
US-09-134-001C-3945
US-09-134-001C-3945
US-09-548-372D-51
US-09-548-372D-51
US-09-548-372D-53
US-09-548-372D-6
US-09-548-372D-6
US-09-548-372D-6
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US-09-548-372D-6
US-09-548-372D-6
US-09-548-372D-73
US-09-548-372D-73
US-09-548-372D-73
US-09-548-372D-73
US-09-134-001C-3790
US-09-134-001C-4588
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US-09-134-001C-5111
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US-08-755-587-184
US-09-173-581-2
                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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US-09-071-035-314
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US-09-441-039-2
                                                                                                                                                                                                                                     262574 seqs, 29422922 residues
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           GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
                                                               using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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1615
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Match Length DB
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886.7
866.7
866.7
867.7
84
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Perfect score:
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11;

Gaps

28;

Length 332;

99

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1 VEPY----QLEGRQAQILKHHYNSLVAENAMKPVSLQPREGEWNWEGADKIVEFARKHNM 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 VEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPVG--PVTGSLYHLGADKKVKM-HESNI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 AIA-NGLAWSNDLKKMYYID-SGKRRVDEYDYDASTLSISNQRPLFTFEKH---EVPGYP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 ELRFHTLVWHSQVPEWFFIDENGNRMVDETDPEKR--KANKOLLLERMENHIKTVVERYK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 P---EVLLDTVK-----IPDPQV---TSVAFGGPNLDELHV----TSAGLQLDDSSLD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 D------GQTIDEEGNL----WVAVFQGQRIIKI-------STQQ
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dery, Claude V
PAPLICANT: Beaulieu, Carol
TILLE OF INVENTION: Thermostable Xylanase DNA, Protein and
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                                                                                                                                                            Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                    83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Sterne, Kessler, Goldstein & Fox P.L.L.C.
1100 New York Ave., NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 5.8%; Score 93; DB 4; Best Local Similarity 24.7%; Pred. No. 0.089; Matches 60; Conservative 36; Mismatches 8
                                                                ATTORNEY/AGENT INFORMATION:
NAME: MUTASHIGG, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4615-0057.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/282,197C
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
    UMBER: US/08/501,126
29-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-282-197C-55; Sequence 55, Application US/08282197C; Patent No. 5871730; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ryszard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                     TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cimbala, Michele A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                             LENGIH: 396 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                amino acid
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                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 KSL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 MSL 306
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                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                          US-08-501-126-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 VSNSHGGNQLDGKSNQYKSVHDMIKDVSPAIV-GVINMQKSTNLDDLFNGKASKSKEAGI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 GSGVIYQISDGSAYIVTNNHVVDGASEIKVQLHNSKQVDAKLIGKDALTDIAVLKIKDTK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----GLAWSNDLKKMYYIDSGKRRVDEYDYDASTLSIS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 GIKAIQFANSSKVQTGDSVFAMGNPLGLEFANS------VTSGIISASERTIDANTSAGN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NORPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLLDTVKIPDPQV 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---VGINSMKIAAAQV 277
                                                                                                                                                                                                                                                                                                                                                                                  --SLEREIAIL-- 82
                                                                                                                                                                                                                                                                                                                                                                                                                        6 EKNOHHYRNSSOKRHTFPWIKTIIVAII--AGIIGALLVLGIGKLLNKTGFNNEGATVHQ 63
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                   ; Score 94; DB 4; Length 413;
; Pred. No. 0.074;
46; Mismatches 101; Indels 114;
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 PVGPV----TGSLY-----HL--GADK-KVKMHESN-----TGSLY
                                                                                                                                                                                                                                                                                                 Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | |: :|: || | :: |: |: |: |: |
EGIGFAIPS-NEVRVIEQLVKHGKIERPSIGIGLIN 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 TSVAFGGPNLDELHVTSAGL----QLDDSSLDKSLVN 287
                                                                                                                                                                                                                                                                                                                                                                                  36 EKTFHKY-VPSOKKYTFCKVDKLVSFIIPLAGSPGRFVV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ALKALI-TOLERANT XYLANASES
                FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11.08

PRIOR FILING DATE: 1997-11.08

PRIOR FILING DATE: 1997-08-14

NUMBER: OF SEQ ID NOS: 5674

LENGTH: 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herweijer, Margaretha A.
Van Beckhoven W.C., Rudolf F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Morrison & Foerster
2000 Pennsylvania Avenue, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herbes, Wilhelmina T.
Van Der Kleij, Wilhelmus A.
                                                                                                                                                                                                                                            ORGANISM: Staphylococcus epidermidis US-09-134-001C-5111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Van Solingen, Pieter
Williams, Diane P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08501126
Patent No. 6140095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Farrell, Roberta L.
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                                                                                                                                                                                                                                                                                                       5.8%;
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                                                                                                                                                                                                                                                                                                       Query Match 5.8%
Best Local Similarity 22.6%
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            verson, Sara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20006-1812
COMPUTER READABLE FORM:
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US-08-501-126-2
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GENERAL INFORMATION:

APPLICANT: UDAKA, Shigezo
APPLICANT: SAKAGUCHI, Kenji
APPLICANT: SAKAGUCHI, Kenji
APPLICANT: YAMAGATA, Hideo
APPLICANT: PANGATA, Hideo
APPLICANT: PREKER, Koen
TITLE OF INVENTION: XYLOSEISOMERASE GENE OF THERMUS
TITLE OF INVENTION: FRUCTOSE
TITLE OF INVENTION: FRUCTOSE
TITLE OF INVENTION: FRUCTOSE
TITLE OF INVENTION: AGUATICUS, XYLOSEISOMERASE AND PROCESS FOR PREPARATION OF
TITLE OF INVENTION: FRUCTOSE
CORRESPONDENCE ADDRESS:
ADDRESSEE: BUINS, Doane, Swecker and Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
         664 MPNQRKVMLAWMTNWDYPFEFPTSSWKGO--LTIPREVSLRTTBEGVRLVQTPITELQKL 721
                                                                         -----VNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPVGPVTGSLYHLGADKK 148
                                                                                                       149 VKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLSISNQRPLFTFEKHEVP 208
                                                                                                                                                                                         209 GYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLLDTVKIPDPQVTSVAF---GGPNLD 265
                                                                                                                                                                                                                                                                                            813 LKPENOKVK-----LRIFVDESSVEVFGNDGKVVFSDVIFPDPAGRAMAFYSLGG---- 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---PS 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 0S/08/112,630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.5%; Score 89.5; DB 1;
19.8%; Pred. No. 0.21;
ive 57; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/783,150
FILING DATE: 28-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08112630 Patent No. 5411886
                                                                                                                                                                                                                                                                                                                                            ELHVTSAGLQLDDSSLDKS 284
                                                                                                                                                                                                                                                                                                                                                                                     863 EVKVSSMKVYALDNIWRKS 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 440 580
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Alexander STATE: Virginia COUNTRY: United States ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.5
Best Local Similarity 19.8
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-112-630-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P---EVLLDTVK-----IPDDPQV---TSVAFGGPNLDELHV----TSAGLQLDDSSLD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303
                                                                                                                                                                                                                                                                                                                                                          100 VEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLP--VGPVTGSLYHLGADKKVKM-HESNI 156
                                                                                                                                                                                                                                                                                                                                                                                                     71 VEPY----QLEGRQAQILKHHYNSLVAENAMKPESLQPREGEWNWEGADKIVEFARKHNM 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 AIA-NGLAWSNDLKKMYYID-SGKRRVDEYDYDASTLSISNQRPLFTFEKH---EVPGYP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ...-STQQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 PSKRDDLYNLVKDLLEQGVPIDGVGHQSHIQIGWPSIEDTRASFEKFTSLGLDNQVTELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 VPSQKKYTFCKVDKL-VSFIIPLAGSPGRFVVSLEREIAILTWD-GVSAAPTSIEAI---
                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                   64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Moller, Soren
APPLICANT: Johansen, Charlotte
APPLICANT: Johansen, Charlotte
APPLICANT: Schafer, Thomas
APPLICANT: Schafer, Thomas
APPLICANT: Schafer, Thomas
APPLICANT: Gergaard, Peter Rabbek
APPLICANT: Hoeck, Lisbeth Hedegaard
TITLE OF INVENTION: A 2,6,-b-D-Fructan Hydrolase Enzyme
TITLE OF INVENTION: Process For Using The Enzyme
TITLE OF INVENTION: Process For Using The Enzyme
TITLE OF INVENTION: 1990-05
FILE REFERENCE: 5540.200-05
CURRENT FILING DATE: 1998-09-17
EARLIER PILING DATE: 1998-09-17
EARLIER PILING DATE: 1998-12-08
EARLIER PILING DATE: 1998-10-08
EARLIER FILING DATE: 1998-09-24
EARLIER FILING DATE: 1998-09-24
EARLIER FILING DATE: 1998-09-24
EARLIER FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.6%; Score 90; DB 4; Length 1277;
21.2%; Pred. No. 1.3;
tive 44; Mismatches 102; Indels
                                                                                                                                                                                                                                                                     5.6%; Score 91; DB 2; Length 397; 24.7%; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D-----GQTIDEEGNL----WVAVFQGQRIIKI-----
                                                                                                                                                                                                                                                                                                                   Mismatches
33,851
ER: 1050.0410000
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09397885 Patent No. 6323007
  REGISTRATION NUMBER: 33,851
REFERENCE/POCKET NUMBER: 1050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 55: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Paenibacillus pabuli
US-09-397-885-3
                                                                                                                                                         LENGTH: 397 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Conservative
                                                                                                                                                                                                                                                                                                                60; Conservative
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Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 KSL 285
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                                                                                                                                                                                                                         US-08-282-197C-55
                                                                                                                                                                                                TOPOLOGY:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ALZHELMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT FILING DATE: 2000-04-12
CURRENT FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR APLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APLICATION NUMBER: US 60/10-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR APLICATION NUMBER: DS 60/101,594
PRIOR FILING DATE: 1999-09-23
                                                                                                                                                                   TITLE OF INVENTION: FIBEONECTIN AND FIBRINGEN BINDING PROTEIN FROM GROUP A TITLE OF INVENTION: STREPTOCOCCI FILE REFERENCE: 022927-008
CURRENT APPLICATION NUMBER: US/09/327,536
CURRENT FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: US 08/714,402
PRIOR APPLICATION NUMBER: US 08/714,402
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 GNLWV---AVFQGQRIIKISTQQP------EVLLD-----TVKIPDPQVTSVA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 FGGPN--LDELHVTSAGL-----QLDDSSLDKSLVNGHVYRV----TGLGVKGFAG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            780 KFISGSGNEWSFEFKNL------KKY-----KKY-----NGTGNDI 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 MAIDAGLPVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYDASTLSI--SNQRPLFTF-----EKHEVPG-----YPDGQ-----TIDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 KYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSLEREIAI -----LTWDGVSAAPTSIEAIVNVEPHIKNNR----LNDGKADPLGNLWTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           807 IYSVKEVTVPTGYDVTYSANDIINTKREVITQQGPKLEIEETLPLESGASG-----GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.4%; Score 88; DB 4; Length 1161; Best Local Similarity 17.5%; Pred. No. 1.9; Matches 64; Conservative 55; Mismatches 122; Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 51, Application US/09548372D Patent No. 6420534
. Application US/09327536
6355477
                                                    Patent No. 6355477
GENERAL INFORMATION:
APPLICANT: FISCHETTI, Vincent A.
APPLICANT: ROCHA, Claudia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1161
TYPE: PRT
CRGANISM: SFFBP gene
US-09-327-536-2
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US-09-548-372D-51
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Patent No. 6380370
GENERAL INFORMATION:
FOR A PAPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BFIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :: | :: | :: | :: | SALKAAFFLADAHALRTEDEEG-VWAFARGCMRTYLILKERAEAFR 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375 SFCNGDKIGALTDRNGLRPGRYTITKDNFIVFSSEVGVIDVPEENVAF------KGQL 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SNDLKKMYYIDSGKRRVDEYDYDASTLSISNQRPLFTFEKHEVPGYPDGQTID 217
                                                                                                                                                                   80 AILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPVGPVTGS 139
                                                                                                                                                                                                                                                                                                                                                                                          140 LYHLGADKKVKM----HE--SNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 ISNORPLFTFEKHEVPGYPDG-----QTIDEEGNLWVAVFQGQRIIKISTQQPEVLL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E----DPEVKELLAAYYQEDPAALALLGPYSRE---KAEALKRAELPLEAKRRGYALE 372
                                                                                                                                                                                                                                                                                                                        154 ----WDWVREALNFMAAYAEDQGYGYRFALEPKPNEPRGDIYFAT------VGSMLAF 201
                        -----FIIPLAGSPGRFVVSLE-----REI 79
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Best Local Similarity 22.8%; Pred. No. 2.6;
Matches 54; Conservative 29; Mismatches
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3945
                                                                                                                             46 QKKYTFCKVDKLVS------
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US-09-327-536-2
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GENERAL INC. 07-203-4

GENERAL INC. 07-203-4

APPLICANT: GURNEY ET AL.

TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/548,372D

CURRENT FILING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: US 60/155,493

PRIOR FILING DATE: 1999-09-23

PRIOR APPLICATION NUMBER: US 60/101,594

NUMBER OF SEQ ID NOS: 73

SEQ ID NOS: 73
                                                                                                                                                142 HLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVD------EYDYDAST 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 YYOROLSSTYRDLRKGV--YVPYTQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKF 169
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     112 YYORQLSSTYRDLRKGV--YVPYTQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKF 169
                                                                                                  170 FIN------GSNWEGILGLAYAEIARLCGAGFPLNQSEVLASVGGSMI 211
                                                                                                                                                                                              212 IGGIDH------SLYTGSLWYTPIRREWYYEVIIVRVEINGODLKMDCKEYNYDKSI 262
                                                  97 IVNVEPHIKNNRLNDGKADPLGNLWTGTMAI------DAGLP-----VGPVTGSLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 FIN------GSNWEGILGLAYAEIARLCGAGFPLNQSEVLASVGGSMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Best Local Similarity 22.0%; Pred. No. 0.55
Matches 63; Conservative 31; Mismatches
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US-09-548-372D-53
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 53, Application US/09548372D Patent No. 6420534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 53, Application US/09548367D Patent No. 6440698
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US-09-548-367D-53
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US-09-548-372D-53
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APPLICANT: GURNEY ET AL.
TITLE OF INVENTORN: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 29915/6280H
CURRENT APPLICATION NUMBER: US/09/548,367D
CURRENT FILING DATE: 1990-09-23
PRIOR FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 73
SSOFWARE: PALENTIN VERSION 3.1
                                                                                                                                                                                                                                                                          Gaps 15;
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                                                                                                                                                                                                                                                                       97;
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                                                                                                                                                                                                                       DB 4; Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L--SISNQR-PLFTFE----KHEVPGYPDGQTIDEEGNLWVA 225
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                                                                                                                                                                                                                                                                     95; Indels
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                                                                                                                                           ; OTHER INFORMATION: Hu-Asp2(b) delta TM
US-09-548-372D-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-548-367D-51; Sequence 51, Application US/09548367D; Patent No. 6440698
                                                                                             ORGANISM: Artificial sequence
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  PatentIn version 3.1
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Best Local Similarity
Matches 63; Conserv
                                                  428
SOFTWARE: Pa
SEQ ID NO 51
LENGTH: 428
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APPLICATE GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 29915/62801
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155, 493
PRIOR APPLICATION NUMBER: US 09/404,133
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                                                                                                                                                                                                                                                                                                                                                          112 YYQRQLSSTYRDLRKGV--YVPYTQCKWEGELGTDLVSIPHGPNVTVRANIAAITESDKF 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GSNWEGILGLAYAEIARLCGAGFPLNQSEVLASVGGSMI 21.1
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                                                                                                                                                     Gaps
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                                                                                                   Length 476;
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                                                                                                   DB 4;
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22.0%; Pred. No. 0.64;
iive 31; Mismatches
                                                                                                 ; Score 86.5; DB
; Pred. No. 0.64;
31; Mismatches
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PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR PELICATION NUMBER: 05 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PALCHIN VERSION 3.1
SEQ ID NO 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 73, Application US/09548372D Patent No. 6420534
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 L--SISNOR-PLFTFE----
                                                                                                      Query Match 5.4%;
Best Local Similarity 22.0%;
Matches 63; Conservative 3
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-6
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Matches 63; Conserv
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APPLICANT: GIRNEY ET AL.

TILLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES;
TILLE OF INVENTION: THEREOF

FILE REFERENCE: 29915/62801

CURRENT APPLICATION NUMBER: US/09/548,372D

CURRENT APPLICATION NUMBER: US/09/548,372D

PRIOR FILING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-24

PRIOR FILING DATE: 1999-09-24

PRIOR FILING DATE: 1998-09-24

PRIOR FILING DATE: 1998-09-24

NUMBER OF SEQ ID NOS: 73

SOFTWARRE: PATENTIN VERSION 3.1

SEQ ID NO 6
                                      ARTILE OF INVENTION: THEREOR
TITLE OF INVENTION NUMBER: US/09/548,367D
CURRENT APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1998-09-24
NUMBER: OF SEQ ID NOS: 73
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 HLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVD-------EYDYDAST 190
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5.4%; Score 86.5; DB 4; Length 434;
Best Local Similarity 22.0%; Pred. No. 0.55;
Matches 63; Conservative 31; Mismatches 95; Indels 97
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; Patent No. 6420534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial sequence
                              GURNEY ET AL
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        GENERAL INFORMATION:
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Sequence 6, Application US/09548367D

Sequence 6, Application US/09548367D

Sequence 6, Application US/09548367D

GENERAL INFORMATION:

APPLICANT: GURNEY ET AL.

TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

TITLE OF INVENTION: THEREFOR

TITLE OF INVENTION: THEREFOR

CURRENT FILING DATE: 29915/6280H

PRIOR FILING DATE: 1999-09-23

PRIOR PLING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 73

SOFTWARE: PALCATION NUMBER: US 60/101,594

NUMBER OF SEQ ID NOS: 73

SEQ ID NO 6

LEARTH: 476

LEARTH: 476
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112 YYQRQLSSTYRDLRKGV--YVPYTQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKF 169
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                                                                 191 L--SISNQR-PLFTFE-----KHEVPGYPDGQTIDEEGNLWVA 225
                                                                                                       191 L.-SISNQR-PLFTFE-----KHEVPGYPDGQTIDEEGNLWVA 225
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US-09-548-367D-6
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US-09-548-367D-6
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Sequence 53, Appl Sequence 53, Appl Sequence 53, Appl Sequence 6, Appli Sequence 15, Appli Sequence 1131, Appli

Sequence 4, Appli Sequence 13724, A Sequence 6, Appli Sequence 2, Appli

Sequence

2, Appli 4, Appli 4, Appli

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Sequence 1 Sequence 6 Sequence 1 Sequence 6 Sequence 2 Sequence 4

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EREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPVGP 135
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US-09-795-847-53
US-09-794-743-53
US-09-794-743-53
US-09-794-925-53
US-09-681-442-53
US-09-681-442-53
US-09-548-366-53
US-09-794-748-6
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US-09-889-414-6
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US-09-889-366-6
US-09-889-414-6
US-09-988-66-6
US-09-988-66-6
US-09-738-626-6960
US-09-738-626-6960
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US-09-870-962-2
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GENEKAL INFUGRALIANI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAMA, JUN

APPLICANT: HORIKAMA, JUN

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIVUKI

APPLICANT: SAKAKI, WASHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NOWBER: US/10/156,761

CURRENT FILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-05-30

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 13272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13272, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
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84; Conservative
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  Query Màtch
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Matches 84;
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ORGANISM:
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12646, A
4495, Ap
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51, Appl
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                                                                                                                                                                      August 1, 2003, 14:35:09 ; Search time 47 Seconds (without alignments) 778.256 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                            1615
1 MGPVVEKIAELGKYTVGEGP......HVYRVTGLGVKGFAGVKVKL 308
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-794-748-51

US-09-794-925-51

US-09-681-442-51

US-09-681-445-51

US-09-68-366-144-51

US-09-68-366-14-51

US-09-68-366-14-51

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Sequence 15, Application US/10160758

Sequence 15, Application US/10160758

Sequence 15, Application US/10160758

Sequence 15, Application US/10160758

Sequence 15, Application No. US2003003607641

GENERAL INFORMATION:

APPLICANT: EXELIXIS, INC.

TITLE OF INFORMATION:

CURRENT FILLING DATE: 2002-06-03

CURRENT FILLING DATE: 2001-06-05

PRIOR APPLICATION NUMBER: US 60/328,605

PRIOR APPLICATION NUMBER: US 60/328,605

PRIOR APPLICATION NUMBER: US 60/357,253

PRIOR FILLING DATE: 2002-02-15

PRIOR FILLING DATE: 2002-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2666 GGPPHWNSLVPVRLQVVPKKVSLPKF--SEPLYTFSAPEDLPEGSEIGIVKAVAAQDPVI 2723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          840 PGSNVHEL-FAIDSESGWITTLQEL-------DCETCQ----TYHFH- 2874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2935 ISEQNRQVTCYITEGDPLGQFGISQVGDEWRISSRKTLDREHTAKYLLRVTASDGKFQAS 2994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         875 VVAYDHGQTIQLSSQALVQVSITDENDNAPRFASEEYRGSVVENSEPGELVATLKTLDAD 2934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 EPHIKNNRLNDGK----ADPLGNLWTGTMAIDAGLPVGPVT-----GSL-YHLGAD 146
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  VTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLSISN 195
                                         124 GGGTLSRLAPDGTARTVLDDVTISNGVGWSPDGRLMYFNDTPTRRIDVFDVDEDGRPV-G 182
                                                                                     254
                                                                                                             QRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLLDTV-KIPDPQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 KKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLSISNQRPLFTFEKHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 VPGYPDGQTI------DEEGNLWVAVFQGQRIIKISTQQPEVLLDTVKIPDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 DKLVSFIIPLAGSPGRFVVSLEREIAIL----TWDGVSAAPTSIEAIVN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.7%; Score 92; DB 15; I Best Local Similarity 21.9%; Pred. No. 30; Matches 80; Conservative 41; Mismatches 140;
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US-09-969-362-3
; Sequence 3, Application US/09969362
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238 TACAFGGAGLTDLYITTA 255
                                                                                                                                                                       255 TSVAFGGPNLDELHVTSA 272
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SOFTWARE: Patentin version 3.1
SEQ ID NO 15
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VTVEI 2999
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98 ------VNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPVGPVTGSLYHLGADKK 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 VPSQKKYTECKVDKL-VSFIIPLAGSPGRFVVSLEREIAILTWD-GVSAAPTSIEAI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       722 RHNLYSAQQMTVGPKSKN-----PLEGLTAGAYEIEAEVEI-PANSSVTEFGFOLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 VKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLSISNQRPLFTFEKHEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.6%; Score 90; DB 10; Length 1277; 21.2%; Pred. No. 7.4;
                                                                                                          TITLE OF INVENTION: A 2,6,-b-D-Fructan Hydrolase Enzyme And TITLE OF INVENTION: Process For Using The Enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Mismatches 102;
                                                                                                                                                   TITLE OF INVENTION: PROCESS FOL USING THE EFFERENCE: 5540.200-US CURRENT APPLICATION NUMBER: US/09/969,362 CURRENT FILING DATE: 2001-10-02 PRIOR PELICATION NUMBER: 09/397,885 PRIOR FILING DATE: 1999-09-17 PRIOR APPLICATION NUMBER: PA 1998 01623 PRIOR APPLICATION NUMBER: 60/101,615
                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/111,675
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKRI, YOSHIVUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12646, Application US/10156761 Publication No. US20030119018A1
                                                     APPLICANT: Ostergaard, Peter Rahbek
APPLICANT: Hoeck, Lisbeth Hedegaard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELHVTSAGLQLDDSSLDKS 284
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Johansen, Charlotte
Schafer, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Paenibacillus pabuli
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HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55; Conservative
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APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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154 SNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLSISNQR--PLFTFEKH--EVPG 209
                                 111 DGKADPLGNLWTGTMAID---AGL-------PVGPVTGSLYHLGADKKVKMHE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 DGQSDGKSSIWTDTFAIDDTASGLRLVSYRLRLTLYRTPGGGITPTVWRLGA----- 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 RRVDEYDYDASTLSISNQRPLFTFEKHEVPGYPD-----GQTIDEEGNLWVAVFQGQRII 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 YPDGQTIDEEGNLWVAVFQGQRIIKISTQQP---EVLLDTVKIPDPQVTSVA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 YDNG-----GEAWCSPTSSQMIIEYWGRRPTPGQLAWVDPSYADPQVCHAA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.4%; Score 87; DB 15; 'Length 450; Best Local Similarity 22.1%; Pred. No. 3; Matches 38; Conservative 23; Mismatches 51; Indels
                                                                                                                                                                                                                                              Sequence 14443, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: SHIRAM, JUN
APPLICANT: SHIRAM, JUN
APPLICANT: SHIRAM, TADAYOSHI
APPLICANT: SHYRAM, AUN
TAPLICANT: SHYORI, YOSHIVKI
APPLICANT: SHYON:
APPLICANT: SHYON:
APPLICANT: SAKAKI, YOSHIVKI
APPLICANT: SHYON:
APPLICANT: BYTORI, WASHIRA
TILLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HAYSHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TREDA, MASATO
APPLICANT: OZAKI, AKI
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6671, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                       EVTNESPROPIG-VGLPDPEHT 558
                                                                                            234 KISTQQPEVLLDTVKIPDPQVT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-738-626-6671
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                                                                                                                                                                                                                                                                               68 PGR-----FVVSLEREIA---ILTWDGVSAAPTSIEAIVNVEPHIK------ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 VAGPENNDTDFTWDEFVRRVNNELANGWGNLVNRTVSM-AHKNFGEVPVPGALEE--SDK 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 YTVGEGPHW-----DHETQTLYFVDTVEKTFHKYV-PSQKKYTFCKVDKLVSFIIPLAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 115; Gaps
                                                                                                                                                                                                        15;
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                                                                                                                                                             DB 15; Length 418;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                           104 IKNNRLNDGKADPLGNLWTGTMAID---AGLPVGPVTG 138
                                                                                                                                                                                                                                                                                                                                                                     40;
                                                                                                                                                          5.5%; Score 89.5; Di
26.5%; Pred. No. 1.5;
                                                                                                                                                                                                        17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/99/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-11-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATCHIN VET: 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4495, Application US/09738626
Publication No. US20020197605A1
                                                                                          ; ORGANISM: Streptomyces avermitilis US-10-156-761-12646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NRKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 21.7%
Matches 70; Conservative
                                                                                                                                                                                Similarity 26.5%
26; Conservative
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12646
LENGTH: 418
                                                                                                                                                        Query Match
Best Local S
Matches 26
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APPLICANT: Parodi, Luis A.
APPLICANT: Parodi, Luis A.
APPLICANT: Van, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
TITLE OF INVENTION: USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 2841/62800 PARODICATION NUMBER: 05/416,901
PRIOR APPLICATION NUMBER: 05/416,901
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-24
PRIOR PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 HLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVD------EYDYDAST 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212 IGGIDH-----SLYTGSLWYTPIRREWYYEVIIVRVEINGODLKMDCKEYNYDKSI 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 IVNVEPHIKNNRLNDGKADPLGNLWTGTMAI------DAGLP-----VGPVTGSLY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 FIN-------GSNWEGILGLAYAEIARLCGAGFPLNOSEVLASVGGSMI 211
                                                                                                                                                  142 HLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVD-------EYDYDAST 190
                                                                                                                                                                            2 GPVVEKIAEL-----GKY---TVGEGPHWDHETQTL-YFVDTVEKTF------HK 41
112 YYQRQLSSTYRDLRKGV--YVPYTQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKF 169
                                                 --DAGLP-----VGPVTGSLY 141
                                                                                                --GSNWEGILGLAYAEIARLCGAGFPLNQSEVLASVGGSMI 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 YVPSQKKYTFCKVDKLVSFIIPLA----GSPGRFVVSLEREIAILTWDGVSAAPTSIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b); OTHER INFORMATION: delta TM US-09-795-847-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97;
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                                                                                                                                                                                                                                                      191 L--SISNQR-PLFTFE----KHEVPGYPDGQTIDEEGNLWVA 225
                                                                                                                                                                                                                                                                                          97 IVNVEPHIKNNRLNDGKADPLGNLWTGTMAI-----
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 51, Application US/09795847 Patent No. US20010018208A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J
APPLICANT: Heinrikson, Robert L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 22.0%
Matches 63; Conservative
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                                                                                                      170 FIN----
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APPLICANT: Van, Riqiang
APPLICANT: Yan, Riqiang
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: 1999-10-27
PRIOR PELICATION NUMBER: 09/49,133
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 GSFVEMVDNLRGKSGQGYYVEMTVGSPP-----QTLNILVDTGSSNFAVGAAPHPFLHR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                     81 ILTWDGVSAAPTSIEAIVNVEPHI--KNNRLNDGKADPLGNLWTGTMAIDAGLPVGPVTG 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97;
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                                                                                                                                                                                                                                                                                                                                  Length 467;
                                                                                                                                                                                                                                                                                                                                                                                   26; Indels
                                                                                                                                                                                                                                                                                                                                    DB 11;
                                                                                                                                                                                                                                                                                                                                  Ouery Match 5.4%; Score 87; DB 18est Local Similarity 35.8%; Pred. No. 3.2; Matches 29; Conservative 10; Mismatches
     PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                           ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 SLYHLGADKKVKMHESNIAIA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : : ||:: | :| | 437 RVGYQPADRRKPMRFNNTAAA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 51, Application US/09794927
Patent No. US20010016324A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gurney, Mark E.
Bienkowski, Michael J.
Heinrikson, Robert L.
Parodi, Luis A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 63; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin V
                                                                                                                                                                                  SEQ ID NO 6671
                                                                                                                                                                                                              LENGTH: 467
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APPLICANT: PATOLI, LUIS A.
APPLICANT: Van, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
TITLE OF INVENTION: USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 28341/62801
CURRENT APPLICATION NUMBER: US/09/794,748
CURRENT APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
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PRIOR FILING DATE: 1998-09-24
SPRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
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CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR PILING DATE: 1999-10-13
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PAPLICANT: Bienkowski, Michael J.
APPLICANT: Heinrikson, Robert L.
APPLICANT: Parodi, Luis A.
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Best Local S
Matches 63
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TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: UNMER: US/09/794,743
CURRENT APPLICATION NUMBER: US/09/794,743
CURRENT FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR PELLING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PATENTIN VOY: 2.0
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263 VDSGTTNLRLPRKVFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQA 308
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Patent No. US20020037315A1
GENERAL INFORMATION:
                                                                                                                                                                             Sequence 51, Application US/09794743 Patent No. US20010021391A1
                                                                                                                                                                                                                                                                                             APPLICANT: Bienkowski, Michael J.
APPLICANT: Heinrikson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang
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Bienkowski, Michael J.
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Best Local Similarity 22.0%
Matches 63; Conservative
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TITLE OF INVENTION: THEREFOR
CURRENT APPLICATION NUMBER: US/09/869,414
CURRENT FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR PALLICATION NUMBER: OF/10599/20881
PRIOR APPLICATION NUMBER: OF/10599/20881
PRIOR PELING DATE: 1999-09-23
PRIOR PELING DATE: 1999-09-24
PRIOR PELING DATE: 1999-09-24
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                              FEATURE:

CTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b)

CTHER INFORMATION: delta TM

US-09-681-442-51
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                                                                                                                                                                                   Length 428;
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1 Similarity 22.0%; Pred. No. 3.2;
63; Conservative 31; Mismatches 95;
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GENERAL INFORMATION: APPLICANT: Beinkowski et al.
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         ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin Ver. 2.0
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US-09-869-414-51
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APPLICANT BLENKOWSKI, Michael J.
TITLE OF INVENTION: ALGHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: OWNBER: US/09/681,442
CURRENT APPLICATION NUMBER: 09/416,901
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-09-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 GSFVEMVDNLRGKSGQGYYVEMTVGSPP-----QTLNILVDTGSSNFAVGAAPHPFLHR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 IVNVEPHIKNNRLNDGKADPLGNLWTGTMAI------DAGLP-----VGPVTGSLY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 FIN------GSNWEGILGLAYAEIARLCGAGFPLNQSEVLASVGGSMI 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 HLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVD-------EYDYDAST 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 YVPSQKKYTFCKVDKLVSFIIPLA - - - - GSPGRFVVSLEREIAILTWDGVSAAPTSIEA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b); OTHER INFORMATION: delta TM US-09-794-925-51
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PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR PILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
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                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                         SOFTWARE: |
SEQ ID NO 51
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                     US-08-633-993A-12
US-08-844-18-12
US-09-378-088A-12
US-09-232-538-5
US-09-427-353-1
US-08-232-538-17
US-08-786-164-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                    US-09-041-886-16
US-09-328-111-304
                                                                                                                                                                                                                                                                                US-08-149-097D-24
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                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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APPLICATION NUMBER: EP 91 114 300. FILING DATE: 26 AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/232,463 FILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/08232463
Patent No. 5670367
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STREET: 1800 Diagonal Road,
CITY: Alexandria
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TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: lin
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STATE:
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42, Appl
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1648, Ap
                                                                                                                        1, 2003, 12:11:42 ; Search time 63 Seconds
   (without alignments)
   4497.926 Million cell updates/sec
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Sequence 8
Sequence 4
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
               version 5.1.6
- 2003 Compugen Ltd.
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US-08-685-811-1
US-09-378-088A-42
US-08-844-188-42
US-08-844-188-39
US-09-378-088A-39
US-09-378-088A-39
US-09-453-702B-206
US-09-453-702B-261
US-09-453-702B-261
US-09-453-702B-261
US-09-453-702B-261
US-08-844-1188-37
US-08-944-1188-37
US-08-378-088A-37
US-08-378-088A-34
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US-09-378-088A-34
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Maximum Match 100%
Listing first 45 summaries
                                                                                     nucleic search, using sw model
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               GenCore
Copyright (c) 1993
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                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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1556 ACTIGGAAGAAGAAGAAGAAGAAGAACATICCCIATICCIAAAGCTITCGITGGCA 1615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 644 CAATTGATGAGGAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCGAATTATAAAA 703
                                                                                                                                                                                                                                                                                                                                                                                        ATCAACGGCCATTATTTACTTTTGAAAAGCATGAAGTGCCTGGATATCCAGATGGTCAAA 643
                                                                                                                                                                                                                                                                                                                                                                                                                      447 AAAAATGCACGAGGAGCAACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAA
                                                                                                                                                                                                                                        464 ACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATATTG
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3.9%; Score 35.8; DB 4; Length 1114;
Best Local Similarity 45.5%; Pred. No. 0.34;
Matches 127; Conservative 0; Mismatches 152; Indels 0.
                                                                                                                                                                 Length 4739;
                                                                                                                                                               Score 42.2; DB 3; Length 4 Pred. No. 0.0076; 0; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    704 TCAGTACCCAACAACGGAAGTGTTACTGGATACCGTAA 742
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VENTION: Pesticidal Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 1999-08-20 PRIOR APPLICATION NUMBER: US 08/633,993 PRIOR FILING DATE: 1996-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08/844,188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Bacillus thuringlensis US-09-378-088A-85
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Cardineau, Guy A.
Schwab, George E.
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PRIOR FILING DATE: 1997 04-18
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PATENTIN VET: 2.0
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Schnepf, H. Ernest
Knuth, Mark
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Best Local Similarity 47.0%;
Matches 131; Conservative (
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Finstad Lee, Stacy
Burmeister, Paula
4739 base pairs
                 TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-378-088A-85
                                                       TOPOLOGY: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1114
                                                                                                            LOCATION:
US-08-685-871-1
                                                                                            NAME/KEY:
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   LENGIH:
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APPLICANT:
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                                                         268 GCACCTACAAGCATAGAAGCTATTGTTAATGTCGAACCACACATTAAAAATAACAGACTC 327
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                                                                                                                                  AATGATGGCAAAAGCAGATCCCCTTGGCAATCTATGGACAGGTACAATGGCTATTGACGCT
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                       Gaps
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                       Mismatches 167; Indels
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Patent No. 6013499
GENERAL INFORMATION:
APPLICANT: NARUMIYA, Shuh
APPLICANT: INAMATSU, Akihiro
TITLE OF INVENTION: RHO TARGET PROTEIN KINASE P160
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          628 TATCCAGATGGTCAAACAATTGATGAGGAGGGTAA 662
   Pred. No. 0.0039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION NUMBER: 28/08/685,871
FILING DATE: 24-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: JP 8-184102
FILING DATE: 25-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-262553
FILING DATE: 14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29,768
                       Conservative 211;
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     4.38;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
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CITY: Washington
STATE: D.C.
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     Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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US-08-685-871-1
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                                                                                                                                                  738 ATTAGGATTTCAAATATAGATTCAGGAATGAAATTTGATATACCAGAAGTAGGTGG 797
                                                                                                                                                                                                                                    798 AGGTACAGATGAAATAAAAACACAACTAAATGAAGAATTAAAAATAGAATATAGTCATGA 857
                                                  507 GAAAAIGIATIATATIGATICGGGGAAAAGAAGAGIAGACGAGIACGATIATGAIGCTIC
                                                                                                         567 TACATTATCCATCAGCAATCAACGGCCATTATTTACTTTTGAAAAGCATGAAGTGCCTGG
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3.9%; Score 35.8; DB 4; Length 1
Best Local Similarity 45.5%; Pred. No. 0.36;
Matches 127; Conservative 0; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                   687 ACAGCGAATTATAAAATCAGTACCCAACAACCGGAAGT 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/378,088A CURRENT FILING DAFE: 1999-08-20 PRIOR APPLICATION NUMBER: US 08/633,993 PRIOR FILING DATE: 1996-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dojillo, Joanna
TITLE OF INVENTION: Pesticidal Proteins
FILE REFERENCE: MA703C2
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 42, Application US/09378088A
Patent No. 6372480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Bacillus thuringiensis
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OTHER INFORMATION: Undetermined
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Cardineau, Guy A.
Schwab, George E.
Michaels, Tracy E.
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Schnepf, H. Ernest
Knuth, Mark
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Burmeister, Paula
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PRIOR FILING DATE: 1997-04-1
NUMBER OF SEQ ID NOS: 130
SOFTWARE: Patentin Ver. 2.0
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US-09-378-088A-42
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                                                                                                                                                                  ATATCCAGATGGTCAAACAATTGATGAGGAGGGTAATTTATGGGTTGCCGTTTTCCAAGG
                                     567 TACATTATCCATCAGCAATCAACGCCCATTATTTACTTTTGAAAAGCATGAAGTGCCTGG
                                                                                                                        738 ATTAGGATTTCAAATCAATATAGATTCAGGAATGAAATTTGATATACCAGAAGTAGGTGG
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35.8; DB 3;
Pred. No. 0.35;
0; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Schnepf, H. Ernest
APPLICANT: Knuth, Mark
APPLICANT: Pollard, Michael R.
APPLICANT: Cardineau, Guy
APPLICANT: Cardineau, Guy
TITLE OF INVENTION: Pesticidal Toxins
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/633,993
FILING DATE: 19-APR-1996
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 42, Application US/08844188 Patent No. 6127180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: SANGERS, JAY M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEPAX: 352-375-800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Narva, Kenneth E.
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Best Local Similarity 45.5
Matches 127; Conservative
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STRANDEDNESS: single
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PRIOR APPLICATION DATA:
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ZIP: 32606-6669
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1581 AGGTACAGATGAAATAAAAACACAACTAAATGAAGAATTAAAAATAGAATATAGATTAGA 1640
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                                                                                                1521 ATTAGGATTTCAAATCAATATAGATTCAGGAATGAAATTTGATATACCAGAAGTAGGTGG 1580
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447 AAAAATGCACGAGGGAACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAA
                                     1401 AAAATATCAATATTGGCAACGAGCAGTAGGAAGTAATGTAGCTTTACGTCCACATGAAAA
                                                                           507 GAAAATGTATTATTTGGGGGAAAAGAAGAAGAGTAGACGAGTACGATTATGATGCTTC
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CURRENT APPLICATION NUMBER: US/09/378,088A
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PRIOR FILING DATE: 1996-04-19
PRIOR APPLICATION NUMBER: US 08/844,188
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dojillo, Joanna
/ENTION: Pesticidal Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 39, Application US/09378088A patent No. 6372480
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Schnepf, H. Ernest
Knuth, Mark
Pollard, Michael R.
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Best Local Similarity 45.5%;
Matches 127; Conservative
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Schwab, George E.
Michaels, Tracy E.
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Burmeister, Paula
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1996-0
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LENGTH: 2132
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      GAAAATGTATTATTGATTCGGGGAAAAGAAGAGTAGACGAGTACGATTATGATGCTTC
                                                                                                        765 AAAATCATATACTTATGAATGGGGCACAGAAATAGATCAAAAAACAACAATTATAAATAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEE: Saliwanchik, iloyd & Saliwanchik
: 2421 N.W. 41st Street, Suite A-1
Gainesville
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APPLICANT: Knuth, Mark
APPLICANT: Pollard, Michael R.
APPLICANT: Cardineau, Guy
APPLICANT: Schwab, George E.
TITLE OF INVENTION: Pesticidal Toxins
NUMBER OF SEQUENCES: 45
ADDRESSERP
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NAME: Sanders, Jay M.
RECISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-703C1
TELECOMMUNICATION INFORMATION:
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FILING DATE: 19-APR-1996
CLASSIFICATION: 435
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,188
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 39, Application US/08844188 Patent No. 6127180 GENERAL INFORMATION:
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Best Local Similarity 45.59
Matches 127; Conservative
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PRIOR APPLICATION DATA:
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APPLICANT: Schnep
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NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
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LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEBATURE:
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LOCATION: 88050. 88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
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LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
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LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
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INFORMATION: polymorphic fragment 5-127-261
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INFORMATION: polymorphic fragment 5-124-273
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                 NAME/KEY: allele
LOCATION: 108308
OTHER INFORMATION: 5-135-357
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INFORMATION: 5-148-352
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OTHER INFORMATION: 5-140-120
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OTHER INFORMATION: 5-140-348
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OTHER INFORMATION: 5-136-174
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INFORMATION: 5-140-361
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OTHER INFORMATION: 5-145-24
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NAME/KEY: allele
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LOCATION: 146345
OTHER INFORMATION:
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INFORMATION:
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LOCATION: 134374
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OTHER INF
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APPLICANT: BOUGUELEREL, Lydie
TITLE OF INVENTION: AN UNCLETC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT PILING DATE: 1999-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-10-06-30
PRIOR FILING DATE: 1998-12-10
NUMBER OF SCO ID NOS: 140
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OTHER INFORMATION: 99-1442-224
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OTHER INFORMATION: 99-1437-325
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LOCATION: 108149
OTHER INFORMATION: 5-135-198
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OTHER INFORMATION: 5-135-155
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OTHER INFORMATION: 5-129-144
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OTHER INFORMATION: 5-130-257
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OTHER INFORMATION: 5-131-395
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OTHER INFORMATION: 5-128-60
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SEQ ID NO 1
LENGTH: 162450
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LOCATION: 88073
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158 AAGTAGATAAACTGGTTTCTTTCATTATTCCCCTTGCT 195
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                         RESULT 9
US-09-434-408-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 AGTATACGGTIGGAGAAGGTCCTCACTGGGATCATGAAACTCAGACCTTATATTTCGTCG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
       NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: allele
LOCATION: 108127..108177
COCHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
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                                                                                                                                                                                                                                                                                                      ON: 99075..99121
INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID35
                                                                                                               SEQ ID33
                                                                                                                                                                                                                                    ION: 99075..99121
INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
                                                                                                                                                                                 SEQ ID54
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Pred. No. 5.3;
0; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: polymorphic fragment 5-135-155
                                                                                                                                                                   OTHER INFORMATION: polymorphic fragment 5-129-144 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                        INFORMATION: polymorphic fragment 5-130-276
                                                                                                               INFORMATION: polymorphic fragment 5-129-144
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Best Local Similarity 51.3%;
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
                                                                                               97130..97177
                                                                              NAME/KEY: allele
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950 INGAYGCNGARMGNCARMGNYINCARGARCARYINAARCARACNGARCARAAYATHWSNW 1009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGATCCCCTGGCCGTTTTGTAGTCAGTTTGGAACGTGAAATAGCCATTCTTACATGGGAT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 GCCGTTAGTGCTGCACCTACAAGCATAGAAGCTATTGTTAATGTCGAACCACACTTAAA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 TACAATGGCTATTGACGCTGGTCTCCCCGTAGGACCGGTCACTGGCAGTTTATATCATTT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : :: : || |:: || |:: || 650 ARTAYYTNYTNCCNATHYTNGARCARGGNATHGARAAYWSNMGNGAYWSNGCNGAYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 AATAAC-----AGACTCAATGATGGCAAAGCAGATCCCCTTGGCAATCTATGGACAGG
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Sequence 3 Application US/09434408
Patent No. 6440697
GENERAL INFORMATION:
APPLICANT: Venezia, Domenick
TITLE OF INVENTION: RING FINGER PROTEIN ZAPOP3
FILE REFERENCE: 98 4.1
CURRENT APPLICATION NUMBER: US/09/434,408
CURRENT FILING DATE: 1999-111-04
EARLIER PLICATION NUMBER: US 60/108,258
EARLIER FILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 2169
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LOCATION: (1)...(2169)
OTHER INFORMATION: n = A,T,C or G
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TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13988 GGAATATICATAATTAATGATTACGTGAGTTTCCAATGGCTAATGGTATTGAATTTAATC 13929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           455 ACGAGAGCAACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAATGT 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     515 ATTATATTGATTCGGGGAAAAGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTAT 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               575 CCATCAGCAATCAACGCCCATTATTACTTTTGAAAAGCATGAAGTGCCTGGATATCCAG 634
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                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                               Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: NO. 6365723el Sequences of
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILLING DATE: 03-Dec-1999
CLASSIFICATION: CURROWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 206: US-09-453-702B-206
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Pred. No. 7.
                                                                                                                                                                                                                             ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
                                                                             APPLICANT: Blattner, Frederick R.
                   Sequence 206, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13868 TAACGCAAAAAATTC 13853
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STRANDEDNESS: double
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Best Local Similarity 45.7
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 53701-2113
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US-09-453-702B-206/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               575 CCATCAGCAATCAACGCCCATTATTTACTTTTGAAAAGCATGAAAGTGCCTGGATATCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     455 ACGAGAGCAACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTGAAGAAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14950 GTGAACTTACATCGTCTAAGAATAGAGTAGAAAGGAAGCTGTTGTACAGTACTATTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         515 ATTATATTGATTCGGGGAAAGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTAT
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                                                                                                                                                                                                                       E. coli 0157
                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
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                                                                                                                                                                              Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.6%; Score 33.6; DB 4; 145.7%; Pred. No. 7.2;
tive 0; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLGGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 261:
US-09-453-702B-261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

**APPLICATION UNMBER: 60/110,955

FILING DATE: 04-DEC-1998

ATTORNEY/AGENT INFORMATION:
sequence 261, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
                                                                                      APPLICANT: Blattner, Frederick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (608) 251-5000
(608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                      Nicole T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14770 TAACGCAAAAAATTC 14755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        695 TTATTAAAATCAGTAC 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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Best Local Similarity 45.79
Matches 117; Conservative
                                                                                                                                         Perna, Ni
Plunkett,
                                                                                                                                                                                                                                                                                                                                                CITY: Madison
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447 AAAAATGCACGAGAGCAACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTGAA 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    627 ATATCCAGATGGTCAAACAATTGATGAGGAGGGTAATTTATGGGTTGCCGTTTTCCAAGG 686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1152;
                                                                                                                           COMPUTER NEALLINE TREPLY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RIING DATE:
CLASSIFICATION NUMBER: US 08/633,993
FILING DATE:
PLING DATE:
CLASSIFICATION NUMBER: US 08/633,993
FILING DATE:
RECISTERION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
RECISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-703C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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44.9%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 152;
:: Saliwanchik, Lloyd & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37, Application US/09378088A Patent No. 6372480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cardineau, Guy A.
Schwab, George E.
Michaels, Tracy E.
Finstad Lee, Stacy
                                     CITY: Gainesviller
STATE: FL
COUNTRY: USA
ZIP: 32606-6669.
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Knuth, Mark
Pollard, Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: DNA (genomic) US-08-844-188-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schnepf, H. Ernest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Narva, Kenneth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1152 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.5'
Best Local Similarity 44.9'
Matches. 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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APPLICANT: Narva, h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-378-088A-37
    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                        GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 CCTGGCCGTTTTGTAGTCAGTTTGGAACGTGAAATAGCCATTCTTACATGGGATGGCGTT.261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 AGTGCTGCACCTACAAGCATAGAAGCTATTGTTAATGTCGAACCACACATTAAAAATAAC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     643 GATATTACAGGITCTATCATTGCTGGTGTGTCAAAGCTGACCTCTATGAAAACTTTACG 702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 AGACTCAATGATGGCAAAGCAGATCCCCTTGGCAATCT 359
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
OPERATING SYSTEM: MSDOS version 6.2
CNERNARE: ASCIT Text
CNREMT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Schnepf, H. Ernest
APPLICANT: Knuth, Mark
APPLICANT: Pollard, Michael R.
APPLICANT: Cardinedu, Guy
APPLICANT: Schwab, George E.
TITLE OF INVENTION: Pesticidal Toxins
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33.2;
Pred. No. 2:
                                                                                                                                                                                               ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                Sequence 244, Application US/08961527
Patent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 37, Application US/08844188
Patent No. 6127180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 36,373
TELECOMMUNICATION INFORMATION:
TELEDHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 244:
SEQUENCE CHARACTERISTICS:
LENGTH: 1052 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Narva, Kenneth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.6'
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
US-08-961-527-244
                                                                                                                                                                                                                                                               STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                       20850
                                 US-08-961-527-244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTAGGATTTCAGATTAATATAGATTCGGGAATGAAATTTGATATACCAGAAGTAGGTGG 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATAICCAGAIGGTCAAACAAITGAIGAGGAGGGTAAITIAIGGGIIGCCGIIITICCAAGG 686
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                            Length 1152;
                                                                                                                                                                                                                                                                                                                                                     Score 32.8; DB 4; Length 1)
Pred. No. 2.7;
0; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACAGCGAATTATAAAATCAGTACCCAACAACCGGA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACCAAAATAATGGAAAAATATCAGGAACAATCAGA 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Saliwanchik, Lloyd & Saliwanchik
2421 N.W. 41st Street, Suite A-1
APPLICANT: DOJILLO, JOANNA
TITLE OF INVENTION: Pesticidal Proteins
FILE REFERENCE: MA70322
CURRENT APPLICATION NUMBER: US/09/378,088A
CURRENT FILING DATE: 1999-08-20
PRIOR PAPLICATION NUMBER: US 08/633,993
PRIOR FILING DATE: 1996-04-19
PRIOR APPLICATION NUMBER: US 08/844,188
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEC ID NOS: 130
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, H. Ernest
APPLICANT: Knuth, Mark
APPLICANT: Pollard, Michael R.
APPLICANT: Cardineau, Guy
APPLICANT: Schwab, George E.
TITLE OF INVENTION: Pesticidal Toxins
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/844,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34, Application US/08844188
Patent No. 6127180
                                                                                                                                                                                                                                                                                            ; ORGANISM: Bacillus thuringiensis US-09-378-088A-37
                                                                                                                                                                                                                                                                                                                                                       3.5%;
                                                                                                                                                                                                                                                                                                                                                                                              Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS ADDRESSE: Saliwanch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gainesville
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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32606-6669
                                                                                                                                                                                                                                                     LENGTH: 1152
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                                                                                                                                                                                                                                SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     507
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1755 AGGTACAGATGAAATAAAAACACAATTAAACGAAGAATTAAAAATAGAATATAGCCGTGA 1814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1635 AAAATCATATGCTTATGAGTGGGGTACAGAAATAGATCAAAAAAACAACTATCATTAATAC 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1754 ITTAGGATTTCAGATTAATATATAGATTCGGGAATGAAATTTGATATACCAGAAGTAGGTGG 1754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447 AAAAATGCACGAGAGCAACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAA 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       627 ATATCCAGATGGTCAAACAATTGATGAGGGGTAATTTATGGGTTGCCGTTTTCCAAGG 686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 2230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1815 AACCAAAATAATGGAAAAATATCAGGAACAATCAGA 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.5%; Score 32.8; DB 3; I
Best Local Similarity 44.9%; Pred. No. 3.6;
Matches 124; Conservative 0; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 687 ACAGCGAATTATTAAAATCAGTACCCAACAACCGGA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: August 1, 2003, 13:22:13
Job time: 74 secs
                                                                                                                      NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
                            19-APR-1996
                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2230 base pairs
                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                         FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11 MOLECULE TYPE:
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Perfect score:

Title:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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C92731 C92731 Dict
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C92540 C92540 Dict
BJ435579 BJ435579
AI663645 ui99104.7
AV890554 AV890554
BJ435579 BJ435579
BJ402499 BJ402499
BJ161908 RED1371.5
BJ5587 BJ402499
BJ161908 RED1371.5
BJ5587 BJ402499
BJ5587 BJ402574
AV905180 AV905180
BJ56225 RH09865.5
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BJ73083 BJ73080
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BB1601016B20D02.5 Bee Brain Normalized Library, BB16 Apis mellifera cDNA clone BB160016B20D02 5', mRNA sequence.
BI514926
BI514926.1 GI:15365300
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Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apidae: Apis.
I (bases I to 638)
Whitfield(C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L.,
Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.E.
Annotated expressed sequence tags and cDNA microarrays for studies
of brain and behavior in the honey bee
Genome Res. 12 (4), 555-566 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eŭkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
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Department of Entomology
University of Illinois
Tel: 217 265 Goodwin Ave., Urbana, IL 61
Tel: 217 244 3499
Fax: 217 244 3499
Email: generobi@life.uiuc.edu
                    C92540
C92541
C92217
C92217
C92559
BJ40259
BJ402499
BJ161908
BJ55587
AV905180
BJ364230
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BI615830
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BI584695
BI364664
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BI567910
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BG639989
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  honeybee.
  BI514926
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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MEDLINE
COMMENT
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AV401529 AV401529
BI611823 RH18245.5
BI617530 RH47894.5
AJ425659 AJ426659.
BI617627 RH48022.5
                                                                       1, 2003, 12:07:04; Search time 1751 Seconds (without alignments) 8546.333 Million cell updates/sec
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 TTAAACCAAAAAAAAATTATCTCCTGTTACTAATAGTAATGGATTAGCTTGGAATCTTC 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                500 ATTTCAAGAAAATGTATTATATTGATTCGGGGAAAAGAAGAGAGTAGACGAGTACGATTATG 559
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                                                                                                                                                                                                                                                                                                                                                           /note-"Organ: brain; Vector: pT7T3-Pac; Site_1: EcoR1; Site_2: Not1; The BB16 library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups. "
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Award in Functional Genomics to G.E. Robinson and an NSF Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield
                                                                                                                                                                                                                                       /clone="BB160016B20002"
/clone="BB160016B20002"
/clone="BB6 Brain Normalized Library, BB16"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
9
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                                                                                                                                                                                                     European bees,
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                                                                                                                                                                                                                                                                                                                       /dev_stage="adult worker honey bee"
/lab_host="DH10B"
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); Mismatches 299;
                                                                                             02
                                                                                                                                                                 1. 638
/organism="Apis mellifera"
/strain="mixed strains of Eu
/sh. rain="ligustica"
/db_xref="taxon:7460"
                                                                        BACKWARD: ATTAACCCTCACTAAAG
Plate: BBL6016B20 row: D column: (
grape: BR.60016B20 row: D column: (
grape: Br.600016B20 row: B column: (
high quality sequence stop: 638.
                                     PCR PRimers
FORWARD: TAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                             /tissue_type="brain"
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AV401529 Bombyx mori diapause-cancelled embryo p50 76 hr after HC1 treatment (HC1 at 20 hr after oviposition) Bombyx mori cDNA clone e96h0839 T3, mRNA sequence.

AV401529.1 GI:6905181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@nirs.go.jp
method.uni-directional, sequence direction:sequenced from T3 primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 ACGGTTGGAGAAGGTCCTCACTGGGATCATGAAACTCAGACCTTATATTTCGTCGACACC :102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Bombyx mori diapause-cancelled embryo p50 76
hr after HCl treatment (HCl at 20 hr after oviposition)"
/sex="female/male mixed"
/tissue_type="diapause-cancelled embryo"
/dow_stage="76 hr after HCl treatment (HCl at 20 hr after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATAAACTGGTTTCTTTCATTATTCCCCTTGCTGGATCCCCTGGCCGTTTTGTAGTCAGT
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                                                                                                                                                                                                                                                                                                         Eukaryotta; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysla: Bombycoidea; Bombycidea; Bombycidea; Bombyx.

I (bases 1 to 666 Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S. Bombyx mori cDNA (1000) Contact: Mita K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (5'->3')
Project='Silkworm Genome Program in MAFF, and Research for Project='Silkworm's see 'SilkBase', 'Future Program in JSPS'. see 'SilkBase', 'http://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb. Location/Qualifiers
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al Similarity · 56.8%;
200; Conservation
620 TGCCTGGATATCCAGAT
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BI617627
RH48022.Sprime RH Drosophila melanogaster normalized Head pFlc-1
Drosophila melanogaster cDNA clone RH48022 5 similar to regucalcin:
FBan0001803 GO:[] located on: X 1LA3-1LA4;: 08/18/2001, mRNA
                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAGTACCCAACAACAGGGAAGTGTTACTGGATACCGTAAAAATACCAGATCCTCAGGTCA 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          824 AGCTTGACGACAGTTCTTTNGACAAAAGTTTAGTTAATGGGCACGTCTACAGAGTAACAG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAATTGATGAGGAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGGGAGAATTATAAAA 703
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                                                                                                                                                                                                                                                                                                                                                                  148 rgaagcagggrrcrcrgrrcrccrgaacaaggaccacarrgragrcaaacarrrcaarc 207
                                                                                                                                                                                                                                                                                                                                                                                             ACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATATTG 523
       /organism="Salmo salar"
/db_xref="taxon:8030"
/clone="s20C06"
/clone="s20C06"
/tissue_type="spleen"
/dev_stage="adult"
/note="Vector: Stratagene lambda Uni-Zap; country=United
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTCGGGGAAAAGAAGAGTAGAGTACGATTATGATGCTTCTACATTATCCATCAGCA
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                                                                                                                                                                                                                          287 CTATTGTTAATGTCGAACCACATTAAAAATAACAGACTCAATGATGGCAAAGCAGATC
                                                                                                                                                                                                                                           347 CCCTTGGCAATCTATGGACAGGTACAATGGCTATTGACGCTGGTCTCCCCGTAGGACCGG
                                                                                                                                                                                               Gaps
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                                                                                                                                                                 Length 719;
                                                                                                                                                                                               Indels
                                                                                                                           1 others
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                                                                                                                                                                 Score 65.4; DB 9; Pred. No. 2e-07; 0; Mismatches 322;
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Drosophila melanogaster
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                                                                                                                                                                    tch 7.1%;
al Similarity 47.3%;
301; Conservative
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                                                                                                                 Kingdom"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGATICGGGGAAAAGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTATCCATCA 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACCGGTCACTGGCAGTTTATATCATTTAGGGGCTGATAAAAAGGTAAAAATGCACGAGA 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGATCCCCTTGGCAATCTATGGACAGGTACAATGGCTATTGACGCTGGTCTCCCCGTAG 400
                                                                                                                                             47 TTGGAGAAGGTCCTCACTGGGATCATGAAACTCAGACCTTATATTTCGTCGACACCGTAG 106
                                                                                                                                                              160
                                                                                                                                                                                                                                                            TAGATAAACTGGTTTCTTTCATTATTCCCCTTGCTGGATCCCCTGGCCGTTTTGTAGTCA 220
                                                                                                                                                                                                                                                                                                                   GTTTGGAACGTGAAATAGCCATTCTTACATGGGATGGCGTTAGTGCTGCACCTACAAGCA 280
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L (bases I to 719)

Cairney, M. and Taggart, J.

Gene sequences in atlantic salmon (Salmo salar)
BamHI: Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid CDNA library."
                                                                                                                                                                                                                                                                                                                                                                           281 TAGAAGCTATTGTTAATGTCGAACCACATTAAAAATAACAGACTCAATGATGGCAAAG
                                                                                                                                                                                                     AGAAAACTTTTCATAAATATGTACCTTCTCAGAAAAAATACACGTTTTGTAAA-----G
                                                                                                                                                                                                                                153 CCGCCGGCATTAATCGTTATGATTTCAAGCAGAACAAAGTGTACAGGGCTAAAATCGAGG
                                                                                                                  6;
                                                                                       Length 635;
                                                                                                                  Indels
                                                                                      Score 66.4; DB 13;
Pred. No. 1e-07;
0; Mismatches 276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Taggart JB
Institute of Aquaculture
University of Stirling
Airthrey Road, FK9 4LA, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ425659.1. GI:22033827
                                                                                         7.28;
                                                                                                                    Conservative
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Salmo salar
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AJ425659
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                                                                                                                       Matches 261;
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AUTHORS
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C92366 560 bp mRNA linear EST 12-JUL-1999 C92366 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSE652, mRNA sequence.
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1 (bases 1 to 560)

Morlo,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takenoto,K., Yasukawa,H., Williams,J., Maeda,M., Takenchi,I., Ochiai,H. and Tanaka,Y.

The Dictyostellium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               652 GAGGAGGGTAATTTATGGCTTGCCGTTTTCCAAGGACAGCGAATTATTAAAATCAGTACC 711
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  510 GCAAGGTGGGCATATCCAATGGCCTGGCCTGAGATGTCAAGGCCAAGAAGTTCTACTTCA 569
                                                                                                   570 TCGACACCAACAACCACGAGGTATTGGCCTATGACTACAATCAGAGCACCGGCGCGCGTAA 629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:44689"
/clone="SSE652"
/clone_lib="Dictyostelium discoideum SS (H.Urushihara)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     472 ATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATATATTGATTCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   592 CCATTATTTACTTTTGAAAAGCATGAAGTGCCTGGATATCCAGATGGTCAAACAATTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 AAAAGAAGAGTAGGGTACGATTATGATGCTTCTACATTATCCATCAGCAATCAACGG
                                                    TTGATTCGGGGAAAAGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTATCCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: hideko@biol.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٠<u>.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-1-1 Tennoudal, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 65; DB 14;
Pred. No. 2.4e-07;
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99156227
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83 c 104 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dictyostelium discoideum. Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Tsukuba
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11 Similarity 50.4%;
186; Conservative
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Matches 186,
                                                    521
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                  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 655)
Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R., Gonzalez,M., Glarin,H., Haris,N., Li,P., Liao,G.,Misra,S., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="Adult"
/lab_host="DH5-alpha TonA"
/lab_host="DH5-alpha TonA"
/note="Organ: head, Vector: pFlc1; Site_1: XhoI; Site_2:
BamHI: Library was kindly generated by Piero Carninci at
the RIKEN The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RH Drosophila melanogaster normalized Head
pFlc-1"
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                                                                                                                                                                                                                                                                                                                                             Dawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Fate: R1484037,11785087]
Fate: R1480 row: B column: 10
Flate: R1480 row: B column: 10
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RH48022"
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Pred. No. 2.2e-07;
0; Mismatches 278;
                                                                                                                                                                                                                                                    BDGP/HHMI RH Drosophila EST Project
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                                                                                                                                                                                                                                                              Unpublished (2001)
Contact: Stapleton, M. BDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.18;
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C92540 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSE589, mRNA sequence.
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Dictyostellum discoideum.

Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.

Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.

I bases 1 to 639)

Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshida, R., Millams, J., Maeda, M., Takeuchi, T., Ochiai, H. and Tanaka, Y. Milliams, J., Maeda, M., Takeuchi, T., Ochiai, H. and Tanaka, Y. The Dictyostellum developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of development
378 ATCACTAAAAAACTTTTATTAACTGTAACTGTTCCAAATGTCTCAAGGGTCACTTCTTGT 437
                                                         /clone_lib="Dictyostelium discoideum SS (H.Urushihara)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  472 ATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATATTTGATTCGGGG
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                                         772 GCATTIGGCGGTCCGAATTIGGATGAACTGCATGTAACATCTGCTGGTCTTCAGCTTGAC
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Email: hideko@biol.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
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Tel: 81-298-53-4664
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/organism="Dictyostelium discoldeum"
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Pred. No. 2.5e-07;
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University of Tsukuba
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/clone="SSE589"
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99156227
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87 c 120
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Best Local Similarity 50.4%;
Matches 186; Conservative (
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C92540.1 GI:3074416
                                                                                                                       832 GACAGTTCT 840
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                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.

1 (bases 1 to 606)

Morlo, T., Urushihara, H., Salto, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshido, T., Williams, M., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y. The Dictyostellum developmental cDNA project; generation and analysis of expressed sequence tags from the first-finger stage of
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                                                                     GCATTTGGCGGTCCGAATTTGGATGAACTGCATGTAACATCTGCTGGTCTTCAGCTTGAC 831
             ATCACTAAAAAACTTTTATTAACTGTAACTGTTCCAAATGTCTCAAGGGTCACTTCTTGT 390
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/clone="SSF142"
/clone_lib="bictyostelium discoideum SS (H.Urushihara)"
/dev_stage="slug" 194 t
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Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp
PROJECT - Dictyostelium discoideum cDNA project in Japan'
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9915627
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudal, Tsukuba, Ibaraki 305-8572, Japan rel: 81-298-53-4664
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Pred. No. 2.5e-07;
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591

Db 387 ATCACTAAAAAACTTTTATTAACTGTAACTGTTCCAAATGTCTCAAGGGTCACTTCTTGT 446	Db 430 ATCACTAAAAAACTTTTATTAACTGTAACTGTTCCAAATGTCTCAAGGGTCACTTCTTGT	ACTICITGT 489
OY 772 GCATTTGGCGGTCCGAATTTGGATGAACTGGATGTAACATCTGGTGGTCTTCAGCTTGAC 831	OY 772 GCATITGGCGGTCCGAATITGGATGAACTGCAGTGTAACATCTGCTGGTTCACCTTGACTTGACTGAC	CAGCTTGAC 831 SATGGTGAA 549
Qy 832 GACAGTTCT 840 	Oy 832 GACAGTTCT 840 	
RESULT 10 C92417 LOCUS C92417 C92411 C92417 C92411 C92417 C92411 C92417 C92411 C92417 C92411 C92411 C92411 C92411 C92417 C92411 C9241 C92411 C	RESULT 11 C90258 LOCUS C90258 DEFINITION C90258 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium ACCESSION C90258 L GI:3059878 VERSION C90258.1 GI:3059878 EST. CHYOSTELIUM discoideum. ORGANISM Dictyostelium discoideum. ORGANISM Dictyostelium Chox (H. V. Salto, T., Takemoto, H., Yoshida, M., Salto, T., Takemoto, H., Yoshida, M., Williams, J., Maeda, M., Takemoth, I., Ochiai, H. and Tanaka, Y. Williams, J., Maeda, M., Takemoth, I., Ochiai, H. and Tanaka, Y. TITLE Developmental CDNA in Dictyostelium discoideum Institute of Biological Sciences University of Tsukuba Institute of Biological Sciences University of Tsukuba I-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan Tel: 81-298-53-4664 Exa: 81-298-53-4664 Exa: 81-298-53-4664 Email: hideko@biol.tsukuba.ac.jp. Email: hideko@biol.tsukuba.ac.jp. Email: hideko@biol.tsukuba.ac.jp. Email: hideko@biol.tsukuba.ac.jp. FEATURES I. 730 //strain="Marchibar Ax4" //	ST 20-APR-1998 Lyostellum ., Yoshida,M., Zasukawa,H.,
POLYA=NO. FEATURES Location/Qualifiers source /organism="Dictyostelium discoideum" /strain="Ax4" /db_xref="taxon:44689" /clone="SSE888" /clone="SSE888"	/db_xref="taxon:44689" /clone="SS1507" /clone_lib="Dictyostelium discoideum SS /dev_stage="slug" 263 a 101 c 135 g 231 t	(H.Urushihara)"
ss (n.orusninara)	Query Match 7.0%; Score 55; DB 14; Length /30; Best Local Similarity 50.4%; Pred. No. 2.6e-07; Matches 186; Conservative 0; Mismatches 180; Indels	3; Gaps 1;
Ouery Match 7.0%; Score 65; DB 14; Length 679; Best Local Similarity 50.4%; Pred. No. 2.6e-07; Matches 186; Conservative 0; Mismatches 180; Indels 3; Gaps 1;	472	
Qy 472 ATAGCAAATGGGTCGCGTGGAGTAATGATTTGAAGAAATGTATTATATTGATTCGGGG 531	OY 532 AAAGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTATCCATCAGCGATCAACGG	AATCAACGG 591 AATCGTCGT 372
	Qy 592 CCATTATTTACATAAGCATGAAGCCTGGATATCCAGATGGTCAAACAATTGAT	ACAATIGAT 651 ACCATIGAT 429
TTGAT	Qy 652 GAGGAGGGTAATTATGGGTTGCCGTTTTCCAAGGACAGCGAATTATTAAAATCAGTACC	ATCAGTACC 711 TGGTGTCCA 489
	OY 712 CAACAACGGAAGTGTTACTGGATACCGTAAAAATACCAGATCCTCAGGTCACCTCTGTA	ACCTCTGTA 771 ACTTCTTGT 549
	QY 772 GCATTIGGCGGTCCGAATTIGGATGAACTGTAACATCTGCTGGTCTTCAGCTTGAC	CAGCTTGAC 831 GATGGTGAA 609

us-10-089-986-1.rst

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Similarity
                                                                                                                               house mouse.
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AUTHORS
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                                                                                                     BJ435579 Tictyostelium discoideum cDNA linear EST 13-MAR-20
BJ435579 Dictyostelium discoideum cDNA library, VF Dictyostelium
discoideum cDNA clone ddv27g15 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /csc="mat A" library, VF" /csc="mat A" /dev_stage="Growth phase" 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          652 GAGGAGGGRATITATGGGTTGCCGTTTTCCAAGGACAACGAATTATTAAAATCAGTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 ATCACTAAAAAACTTTTATTAACTGTAACTGTTCCAAATGTCTCAAGGGTCACTTCTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    592 CCATTATTTACTTTTGAAAGCATGAAGTGCCTGGATATCCAGATGGTCAAACAATTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472 ATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATTTGATTCGGGG
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                                                                                                                                                                                                                  Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.

1 (bases 1 to 743)

Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.

Full length cDNA of Dictyostellum discoideum at the vegetative
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Pred. No. 2.6e-07;
0; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                      Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Ill1 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="AX4"
/db_xref="taxon:44689"
/clone="ddv27g15"
                                                                                                                                                                                                                                                                                                                                                                                          tshini@genes.nig.ac.jp.
Location/Qualifiers
1. 743
                                                                                                                                                                                           Dictyostelium discoideum
Dictyostelium discoideum
                                                                                                                                                             BJ435579.1 GI:19410301
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Best Local Similarity 50.4%;
Matches 186; Conservative
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                                 610 CCTGATTCT 618
      832 GACAGITCT
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/dev_stage="adult"
//dev_stage="adult"
//dev_s
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The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Ucher_ESTs uighhd x1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
Washington Box 8501, St. Louis, MO 63108, USA
                                                   EST 10-MAY-1999
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555 bp mRNA linear EST 10-MAY-199 u199h04.y1 Sugano mouse liver mlia Mus musculus cDNA clone PRAGE:1890583 5' similar to SW:SM30_MOUSE Q64374 SENESCENCE MARKER AI665845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathl; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:974907
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/strain="C578L"
/db_xref="taxon:10090"
/clone="InMAGE:1890583"
/clone=lib="Sugano mouse liver mlia"
/sex="female"
/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                            513 bp mRNA linear EST 08-MAR-2C BJ371993 Dictyostelium discoideum cDNA library, CF Dictyostelium discoideum cDNA clone ddc10c20 3', mRNA sequence.
BJ371993 BJ371993.1 GI:19281376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 513)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the culmination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="AX4" | /db_xref="taxon:44689" | /db_xref="taxon:44689" | /clone="ddc10c20" | /clone_lib="Dictyostelium discoideum cDNA library, CF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     472 ATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATATTGATTCGGGG
                                                                                   GAGGAGGGTAATTTATGGGTTGC - - - CGTTTTCCAAGGACAGCGAATTATTAAAATCAGT
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   ATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATATTGATTCGGGG
                    AAAAGAAGAGTAGAGTACGATTATGATGCTTCTACATTATCCATCAGCAATCAACGG
                                                                                                                                    CCATTATTTACTTTGAAAAGCATGAAGTGCCTGGATATCCAGATGGTCAAACAATTGAT
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Unpublished (2002)
Contact: Tadasu Shin.i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yates Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
10cation/Qualifiers
113
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Pred. No. 1.3e-06;
O; Mismatches 166;
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103 c 82 g 162 t
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Best Local Similarity 50.9%;
Matches 175; Conservative (
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BJ371993/c
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phibobranchia; Cionidae; Ciona.
1 (bases 1 to 730)
Satch,N., Satcu,Y., Kohara,Y. and Shin-i,T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satch
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA library, cleavage
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                                                                                412 GGCAGTTTATATCATTTAGGGGCTGATAAAAAGGTAAAAATGCACGAGAGCAACATAGCT
                                                                                                                               543 AGACGAGTACGATTATGATGCTTCTACATTATCCATCAGCAATCAACGGCCATTATTTAC
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                                                                                                                                                                                                                                 GATGGAAAAAGATGAACA----AATCCCCAGATGGAATGTGCATTGATGCTGAGGGAAA
                                                                                                                                                                                                                                                                  663 ITTATGGGTTGCCGTTTTCCAAGGACAGCGAATTATTAAAATCAGTACCCAACAACCGGA
                                                                                                                                                                                                                                                                                                                                     AGTGTTACTGGATACCGTAAAAATACCAGATCCTCAGGTCACCTCTGTAGCATTTGGCGG
TCATTTAGGGGCTGATAAAAAGGTAAAAATGCACGAGGAGCAACATAGCTATAGCAAATGG
                               CTCCCTCTTTCCTGATCACAGTGTGAAGAAATACTTTGACCAAGTGGATATCTCCAATGG
                                                              483 GCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATATTGATTCGGGGAAAAGAAGAGG
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Pred. No. 7.5e-07;
0; Mismatches 181; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone="rcicl28p05"
/clone_lib="Nori Satoh unpublished
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/note="Vector: pBluescript SK"
166 c 134 g 233 t
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                         783 TCCGAATTTGGATGAACTGCATGTAACATCTGC 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="whole animal"
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qa	221	221 CATTGTATATCTTTTGAAAACGGTAATTTCGGCTTCCCAGATGGTATGACCATTGAT 165
Qy	652	652 GAGGAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCGAATTATTAAAATCAGTACC 711
qa	164	164 AGTGAAGGTAAACTCTGGATTGCTCATTGGGAGGTGGTAGAGTTACAAGATGGTGTCCA 105
Qy	712	712 CAACAACCGGAAGTGTTACTGGATACCGTAAAAATACCAGATCCTCAGGTCACCTCTGTA 771
qq	104	FAACTGTTC
Qy	772	772 GCATTIGGCGGTCCGAATTIGGATGAACTGCAACGTAACATCTGC 815
qq	44	44 GCTTTTGGTGATTCTGATCTTCATTTTATCACAACTGC 1
Search	Search completed: Au	Search completed: August 1, 2003, 13:20:58

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B. thuringiensis 4
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Human ROCK1 cDNA S
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/transl_except= (pos:782..784, aa:Leu)
/note= "No start or stop codon given"
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Nucleotide sequenc
Drosophila melanog
Rat regucalcin cDN
Mouse SMP30 encodi
Human SMP30 gene.
Senescence marker
Gene #1648 used to
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                 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                        2185239 seqs, 1125999159 residues
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Listing first 45 summaries
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ABL12833
AAQ87295
ABL99968
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AAX40196
ABN95150
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N_Geneseq_101002:*

Database

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

US-10-089-986-1 924

Perfect score:

Sequence:

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Run on:

Scoring table:

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DB

Query Match Length

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                                                                                                                                                                                                                                                    Luciola lateralis luciferin
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                                                                                                                                                            924
                                                                                                                                                                                                                      (first entry)
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556; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kurosawa K,
                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                    1.924
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B; ABB06339.
                                                                                                                                                             standard;
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ABLA971:

AND ABB
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                                                                                                                                  The present sequence is the coding sequence from firefly for a protein that regenerates luciferin by using oxyluciferin and D-cysteine. The encoded protein can be used for regeneration of luciferin, a substrate for luciferase, used for ATP (adenosine triphosphate) assays in both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGTGTTACTGGATACCGTAAAATACCAGATCCTCAGGTCACCTCTGTAGCATTTGGC
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                                                          protein and gene encoding it useful for luciferin from oxyluciferin and D-cysteine
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                                                                                                                                                                                                                                                       Length 865;
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                                                                                                                                                                                                                         Sequence 865 BP; 267 A; 163 C; 195 G; 239 T; 1 other;
                                                                                                                                                                                                                                                     Score 863; DB 22; I; Pred. No. 3.1e-242; 0; Mismatches 0;
                                                                                                        21pp; Japanese
                                                                                                                                                                                                medical and food hygiene areas.
                                                                                                                                                                                                                                                         93.4%;
                                                                                                                                                                                                                                                                                     Matches 864; Conservative
                                                                                                         Page 14-15;
                                                               Luciferin regenerating regenerating expensive
                  2001-266307/27
                                                                                                                                                                                                                                                                        Similarity
                                  P-PSDB; AAB82087
                                                                                                           Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Luciola lateralis-originated genes encoding proteins capable of regenerating luciferin especially from oxyluciferin, useful for producing recombinant DNAs and transformants to give proteins useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a protein capable of regenerating luciferin, which is isolated from Luciola lateralis (Japanese firefly). The gene encoding the protein capable of regenerating luciferin can be used for producting recombinant DNAs and transformants, which can be used for the production of proteins useful in assaying adenosine triphosphate (APP) in medical sciences and food hygiene. The protein can be added to the luciferin-luciferase reaction system to sustain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGGGGCCCAGTTGTTGAAAAATTGCAGAACTTGGCAAGTATACGGTTGGAGAAGGTCCT
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Luciola lateralis; luciferin; regeneration; Japanese firefly; adenosine triphosphate; ATP; medical science; food hygiene; luciferase; luminescence; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Luciferin regeneration protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                   TICCCGGGAGTTAAAGTGAAGCTA 865
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tch 34.7%;
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563; Conservative (
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P-PSDB; ABB09720
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                                                                                             GAACCACACATTAAAAATAACAGACTCAATGATGGCAAAGCAGATCCCCTTGGCAATCTA
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                 ATTATICCCCTIGCTGGATCCCCTGGCCGTTTTGTAGTCAGTTTGGAACGTGAAATAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Luciola cruciata-originated genes encoding proteins capable of regenerating luciferin especially from oxyluciferin, for producing recombinant DNAs and transformants .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a protein capable of regenerating luciferin. The protein can especially regenerate luciferen from roxyluciferin. The protein can be added to the luciferin-luciferase reaction system to sustain luminescence and reduce the amounts used. The polynucleotide sequence is useful for producing recombinant transformants, which are useful for the production of proteins useful in assaying ATP in medical sciences and food hygiene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 24; Length 930;
                                                                             "Luciferin regenerating protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 320.4; DB 24; Length
Pred. No. 2.1e-83;
0; Mismatches 357; Indels
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Location/Qualifiers
1.,930
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3

4

Gaps

18; 912;

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163

280

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TTATTAAAATCAGTACCCAACAACAGGAAGTGTTACTGGATACCGTAAAAATACCAGATC 754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 GACCGGICACTGGCAGTTTATATCATTTAGGGGCTGATAAAAAAGGTAAAAATGCACGAGA 460
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                                                                                                                                                                                                                                                                                                                                                47 TIGGAGAAGGICCICACTGGGAICATGAAACTCAGACCTTATATTTGTCGTCGACACGTAG 106
                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGTCAAACAATTGATGAGGAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 TAGATAAACTGGTTTCTTTCATTATTCCCCTTGCTGGATCCCCTGGCCGTTTTGTAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                     Score 98.6; DB 23; Length
Pred, No. 1.7e-18;
0; Mismatches 379; Indels
                                                                                                                                                                                               Sequence 912 BP; 231 A; 246 C; 238 G; 197 T; 0 other;
                                                                                                                                                                                                                                         10.78;
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Best Local Similarity
Matches 384; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or more cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                             775 TITGGCGGTCCGAATTTGGATGAACTGCATGTAACATCTGCTGGTCTTCAGCTTGACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GTGCTGATGAAACCAATGAAGGTGCTATCTATAAAGTAACTGGACTTGGTG
                                                                                                                                                                                      TTATTTACTTTTGAAAAGCATGAAGTGCCTGGATATCCAGATGGTCAAACAATTGATGAG
                                                                                                                                                                                                                                                                        GAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCGAATTATTAAAATCAGTACCCAA
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                    GCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATATTGATTCGGGGAAA
                                        AGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTATCCATCAGCAATCAACGGCCA
                                                                                                                            Drosophila melanogaster expressed polynucleotide SEQ ID NO 32981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 genes from Drosophila and for elucidating cell signalling and c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 32981; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAGGTTTCGCGGGAGTTAAAGTGAAGCT 923
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                              894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-human animals with defective senescence marker protein 30 function, useful for producing antibody, histopathological diagnosis and onset mechanism of disease due to aging, and in screening side-effects during
                                  SMP30;
655 GAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCGAATTATTAAAATCAGTACCCAA
                                                                                                   715 CAACCGGAAGTGTTACTGGATACCGTAAAAATACCAGATCCTCAGGTCACCTCTGTAGCA
                                                                                                                                   775 TTTGGCGGTCCGAATTTGGATGAACTGCATGTAACATCTGCTGGTCTTCAGCTTGACGAC
                                                                                                                                                                                                                                                      827 TTTGGAGGGAAGGATTACTCTGAAATGTACGTGACATGTGCCAGGGATGGGGATGAGCGCC
                                                                                                                                                                                                                                                                                                           835 AGTICITINGACAAAAGTITAGTIAAIGGGCACGICIACAGAGTAACAGGITTAGGCGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                senescence marker protein 30; cancer; aging; senescence; atic; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse SMP30 encoding cDNA SEQ ID NO 2.
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73..972
/*tag= a
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/product= '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-405445/43.
P-PSDB; ABB83787.
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(KASA/) KASAHARA Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTTTATATATCATTTAGGGGCTGATAAAAAGGTAAAAATGCACGAGAGCAACATAGCTATA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             476 ICCTIGIACTCCCTTTTTCCTGATGACAGTGAGAAATACTTTAACCAAGTGGATATC 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rat liver cDNA clone coding for a calcium binding protein of mc . 33388 was isolated and sequenced (AAQ87295). The protein was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding regucalcin - useful for the recombinant production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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aa:His
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Pred. No. 4.9e-16;
0; Mismatches 292
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/transl_except= pos:500..502,
                                                                                                                                                                                                                           Calcium binding protein; regucalcin; rat; ds.
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                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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(YAMA/) YAMAGUCHI M.
                        BP.
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                     CDNA; 1216
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Best Local Similarity 50.2 Matches 307; Conservative
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/*tag=
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                                                                                                                                                                           Rat regucalcin cDNA.
                  AAQ87295 standard;
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                                                                                                                                                                                                                                                                              Rattus rattus
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                                GTCGAACCACATTAAAAATAACAGACTCAATGATGGCAAAGCAGATCCCCTTGGCAAT 357
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                                                                                                  AGTITIATATCATTTAGGGGCTGATAAAAAGGTAAAAATGCACGAGAGCAACATAGCTATA
                                                                                                               469 rccrigracrccrcrrrrrccrearcacacrcraacraracrrrraaccaagragararc
                                                                                                                                             358 CTATGGACAGGTACAATGGCTATTGACGCTGGTCTCCCCGTA---GGACCGGTCACTGGC
                                                                           409 TACTITGCTGGTACCATGGCTGAGGAAACGGCCCCAGCTGTTCTTGAGCGCACCAAGGG
                  Gaps
                 12;
 Length 1573;
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 Score 80.8; DB 24;
Pred. No. 3.6e-13;
); Mismatches 298;
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/product= SMP30 marker protein
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49.38;
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                    301; Conservative
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           Similarity
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     Query Match
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Matches 3(
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AAQ90035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    835 AGTICTIINGACAAAAGTITAGTIAAIGGGCACGICIACAGAGTAACAGGITIAGGCGTC 894
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                                                                                                                                                                                                                                                                                              AAQ90035 is the SMP30 gene. It encodes the human ageing marker protein, SMP30 (AAR74219). Human SMP30 is found in human organs, tissues, blood, urine and cerebrospinal fluid. The blood concentration of SMP30 is known to increase with renal and hepatic deficiencies and to decrease with age. It is therefore useful in the monitoring of renal or hepatic deficiencies and for the monitoring of the development of the liver and kidneys in newborn bables.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         670 GITTACAAGCTAGAAAAGGAAGAA-----CAAATCCCAGATGGAATGTGTTGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              535 AGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTATCCATCAGCAATCAACGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             595 ITATITACITITGAAAAGCATGAAGTGCCTGGATATCCAGATGGTCAAACAATTGATGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 CTATGGACAGGTACAATGGCTATTGACGCTGGTCTCCCCCG---TAGGACCGGTCACTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                          Novel polypeptide for detecting human ageing marker protein SMP30 for monitoring liver and kidney development in new-born bables
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 74.4; DB 16; Length 1356;
Pred. No. 2.5e-11;
0; Mismatches 302; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1356 BP; 373 A; 274 C; 343 G; 366 T; 0 other;
                                                                                                                                                                                                                                                                 Claim 3; Page 6-7; 10pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 48.6%;
Matches 297; Conservative
93JP-0265681
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||AAAGGAATTGC 971
                                                        (FJRE ) FUJI REBIO KK
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P-PSDB; AAR74219.
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                                                                                                                                                                                                                                                                                                                                                   724 GAGGGGAAGCTCTGGGTGGCCTGTTACAATGGAGGAAGAGTGATTCGTTTAGATCCTGTG 783
                                                                                                                                                                                                                                                                                                                                                                                           CAACCGGAAGTGTTACTGGATACCGTAAAATACCAGATCCTCAGGTCACCTCTGTAGCA 774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene, liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCCTGTACTCCCTCTTTCCTGATCACCACGTGAAAAAGTACTTTGACCAGGTGGACATT
                                                                                          GAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCAATTATTAAAATCAGTACCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vockley JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene #1648 used to diagnose liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1648; 298pp; English.
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961 AAAGGAATTGC 971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAGGTTTCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                 Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer; prostate cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Obata Y, Old
, Stockert E;
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                                                                                                                                             Senescence marker protein SMP30 gene.
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97US-0061765.
97US-0948705.
97GB-0021697.
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97US-0896164
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Sahin U,
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Matches 297; Conservative
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11-OCT-1997
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AAX40196
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26-MAR-2002 (first entry)

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The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver lumbour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN3503-ABN97455 in a cytostatic activity. The method of the invention has hepatocropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver actinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, dung totality, duug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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Pred. No. 2.5e-11;
); Mismatches 302; Indels 12;
                                                                                                                                                                                                                                                                                                       Sequence 1356 BP; 373 A; 274 C; 343 G; 366 T; 0 other;
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Best Local Similarity
Matches 297; Conserv
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ABL12832/c ID ABL12832 standard; CDNA; 2970 BP.

RESULT 10

ABL12832

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GATGCGGTCTTCGTACGGTCATCGTCGAGTGGATGGAGTCTCCGCAGTGGCCAAGGTCA 1688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences (ABLO1840-ABLJ0511), expressed DNA sequences (ABLD1840-ABLJ0511), expressed DNA sequences (ABLD1840-ABLJ0512) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                      NO 32978
                                                  developmental biology; cell signalling; insecticide;
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Pred. No. 5.3e-10;
0; Mismatches 341; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                        English
                    Drosophila melanogaster expressed polynucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2970 BP; 893 A; 558 C; 574 G; 945 T; 0 other;
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320; Conservative
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                                                                                                     Drosophila melanogaster.
                                                        Drosophila; developmer
pharmaceutical; gene;
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11-JUL-2000;
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                                                                                              Gaps
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                                               Length 1086;
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237 T; 0 other;
                                                                                           0; Mismatches 400;
                                            Score 67; DB 23;
Pred, No. 3.3e-09;
C; 296 G;
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GCAACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATA
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                                                                                                                                                                                                                                                                                                                                     detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                       insecticide;
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                     developmental biology; cell signalling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 67; DB 23;
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2000US-0614150.
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Best Local Similarity 46.6
Matches 365; Conservative
                                                                     Drosophila melanogaster
                     Drosophila; developmer pharmaceutical; gene;
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                                                                 Sequence 1119 BP; 266 A; 302 C; 310 G; 241 T; 0 other;
(ABB57737-ABB72072).
The sequence data for this patent did not form part o
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                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
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                                                          Drosophila melanogaster expressed polynucleotide SEQ ID
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Matches 300; Conservative
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                                                                             2019 TCGATACCACCGACTACGAGGTGAAGTCGTATGACTATGATTTCGAGACCGGCGTGGCTA
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                                                       47 TTGGAGAAGGTCCTCACTGGGATCATGAAACTCAGACCTTATATTTCGTCGTCGTAG
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Length 4624;
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 Score 52.8; DB 23;
Pred. No. 9.3e-05;
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Copyright (c) 1993 - 2003 Compugen Ltd.
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a Pred. No. is the number of results predicted by chance to have

609237 CONA insert AB036903 Sarcophag D38467 Rat mRNA fo X69021 R.norvegicu AB037934 Rattus no D86217 Mus musculu U28937 Mus musculu BC012710 Mus musculu AB037936 Xenopus I AX409001 Sequence E09013 CDNA encodi D31815 Human mRNA AB028125 Homo sapi AB033264 Homo sapi AB03368 Xenopus I AP000987 Sulfolobu AC013939 Drosophil AC07808 Brosophil AB062786 Photinus AB072447 Luciola 1 AB072448 Luciola C AY071130 Drosophil AY028616 Calliphor AB022490 Drosophil AF326959 Calliphor AB036904 Drosophil ACL16963 Dlotyoste AB079885 Sarcophag AE006864 Sulfolobu AP000990 Sulfolobu AB037935 Gallus ga AC014187 Drosophil Oryctolag Drosophil Drosophil U05664 Sulfolobus AB035445 Oryctola score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description SUMMARIES RNSMP30A AB037934 D86217 AY071130 AY028616 AB029490 AF326959 E09237 AB036903 HUMSMP30 AB028125 MMU28937 AB033368 AP000987 AX409001 E09013 AB035446 AC007808 RATCBP1 AB032064 SAU05664 10 DB Query Match Length 1394 49817 167195 254961 1040 1150 1022 1216 1155 11594 1594 1605 1109 1573 Score 923 325.2 320.4 98.6 97.2 Result

ALIGNMENTS

164237 7218

AC014187 Drosophil AC023688 Drosophil AE0063487 Drosophil AC023731 Drosophil AX083744 Sequence AP005199 Oryza sat I66494 Sequence 14

AP000990

633 10105

INV 27-SEP-2001 AB062786 927 bp mRNA linear INV 27-SEP-200 Photinus pyralis mRNA for luciferin regenerating enzyme, complete Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia; Cantharoidea; Lampyridae; Photinus. Photinus pyralis cDNA to mRNA. Photinus pyralis AB062786 AB062786.1 GI:14331151 Gomi, K. and Kajiyama, N. AB062786 RESULT 1 AB062786 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

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/translation="MSPVIEOTTEVDNEQIGEGPHMDTETOSLYFVDILEKSIHKYVP
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PETDSYRTKLNKGGLYRTGLGVRGKPESLIGVINNPESLITSVCFGGSKLDELYVTTSGIKE
TETDSYRTKLNKGGLYRTGLGVRGKPARRFSL"
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                                                                                                                                                                                                                                                                                                                                                                      mRNA linear INV 22-FEB-2002 luciferin-regenerating enzyme,
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Gomi,K., Hirokawa,K. and Kajiyama,N.

Gomi,K., Hirokawa,K. and Kajiyama,N.

Submitted (04-0CT-2001) Keiko Gomi, Kikkoman Corporation, Research and Development Division; Noda 399, Noda, Chiba 2780037, Japan (E-mail:8553@mail.kikkoman.co.jp, Tel:81471235579, Fax:81471235550)
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                                            AATTTATGGGTTGCCGTTTTCCAAGGACAGCGAATTATTAAAATCAGTACCCAACAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia; Cantharoidea; Lampyridae; Luciola.
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Molecular cloning and expression of luciferin-regenerating (LRE) cDNa in Luciola cruciata and Luciola lateralis
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/protein_id="BAB85478.1"
/db_xref="G1:18857905"
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Pred. No. 1.1e-70;
); Mismatches 364;
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/db_xref="taxon:7052"
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SQKKYTFCKVDKLVSFIIPLAGSPGRFVVSLEREIALLTWDGVSAAPTSIEAIVNVEP
HIKNNRLNDGKADPFGNLWTGTMAIDAGLPVGPVTGSLYHLGADKKYKMHESNIAIAN
GLAMSNDLKKMYYIDSGKRYNDEYDYDASTLSISNQRPLFTFKHEVPGYPDGQTIDE
EGNLWANDLKGWYIISTQQPEVLLDTVKTPDPQVTSVAFGGPNLDELHVTSAGLQL
DDSSLDKSLVNGHYRTGLGYRGFAGVKVKL"

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          luciferase,
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(bases 1 to 927)

(bases 1 to 927)

Direct Submission

Submitted (07-JUN-2001) Kelko Gomi, Kikkoman Corporation,

& Development; Noda 399, Noda-shi, Chiba 2780037, Japan

(E-mail:8553@mail.kikkoman.co.jp, Tel:81471235579)
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pred. No. 3e-220;
0; Mismatches 1; Indels
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        firefly
oxyquoiferin, a luminescence product of fir enzymatically regenerated into luciferin J. Biol. Chem. 276 (39), 36508-36513 (2001) 21453302
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1. .927
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Local Similarity 99.9%;
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                                                                                                                                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 GACCGGTCACTGGCAGTTTATATCATTTAGGGGCTGATAAAAAGGTAAAAATGCACGAGA 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATA 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  521 TTGATTCGGGGAAAAGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTATCCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAACCCAAAGGTCATCTTCGATCTGAGGAGATTCGGCCCGAAGGACCATTGTTCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 GATGCGGTCTTCGTACGTCATCGTCGGATGGATTCGCCAAGGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 TGGGCGAGGGACCCCACTGGGATGTTGATCGCCAGAGTCTGTACTACGTGGACCTCGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGCCGGCATTAATCGTTATGATTTCAAGCAGAACAAAGTGTACAGGGCTAAAATCGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 TAGATAAACTGGTTTCTTTCATTATTCCCCTTGCTGGATCCCCTGGCCGTTTTGTAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                             /note="alignment with genomic scaffold AE003706"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 98.6; DB 3; Length 10 Pred. No. 5.2e-14; 0; Mismatches 379; Indels
   S
ema11
                                                                                                                    melanogaster'
   send
   (http://fruitfly.berkeley.edu) or
cdna@fruitfly.berkeley.edu.
Location/Qualifiers
                                                                                                                       /organism-"Drosophila
                                                                                                                                            /strain="y; cn bw sp"
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                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Longest ORF"
                                                                                                                                                                                                                                                                 /gene="smp-30"
                                                                                                                                                                                                                                                                                                                                                                                  /gene="smp-30"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;
Nooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophildae; Drosophila.

1 (bases 1 to 1040)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E., George, R., Gonzalez, M., Glarin, H., Kronmiller, B., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            775 TITGGCGGTCCGAATITGGATGAACTGCATGTAACATCTGCTGGTCTTCAGCTTGACGAC 834
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                                                                                                                                                                                                                                                                                                                                                                                                                   661 GAAGGAAACTTATGGGTAGCCACATGTCAAGGTGATAAAAGTTTTAAAAATTGATACTAGT 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                835 AGTICTITNGACAAAAGTITAGTIAATGGGCACGTCTACAGAGTAACAGGTITAGGCGTC
            GCAAATGGGCTCGCCTGGAGTAATGATTTGAAGAAAATGTATTATATTGATTCGGGGAAA
                                             AGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTATCCATCAGCAATCAACGGCCA
                                                                                                                                                            TTATTTACTTTTGAAAAGCATGAAGTGCCTGGATATCCAGATGGTCAAACAATTGATGAG
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Submitted (18-DEC-2001) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
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Drosophila melanogaster RE17477 full length cDNA.
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AUTHORS
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mRNA linear INV 03-MAY-2002 senescence marker protein-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        742 GCCATTCCATCTACAAAATTAATCCCACCACTGGCCAAGTTTTGTTGGAAA---TCAAAT 798
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Drosophila melanogaster (strain:Canton S) 7 day adult stage whole
                                                                                                       TAGATAAACTGGTTTCTTTCATTATTCCCCTTGCTGGATCCCCTGGCCGTTTTGTAGTCA
                                                   205 GTGAGGATTTAGCTGGTTTTGCTGCCCGTCGAAGGTACAACCGATCAATTTGCTGTCG
                                                                                      GTTTGGAACGTGAAATAGCCATTCTTACATGGGATGGCGTTAGTGCTGCACCTACAAGCA
                                                                                                                                                    281 TAGAAGCTATTGTTAATGTCGAACCACATTAAAAAT-----AACAGACTCAATG
                                                                                                                                                                                                                        ATGGCAAAGCAGATCCCCTTGGCAATCTATGGACAGGTACAATGGCTATTGACGCTGGTC
                                                                                                                                                                                                                                                                                      392 TCCCCGTAGGACCGGTCACTGGCAGTTTATATCATTTAGGGGCTGATAAAAAGGTAAAAA
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insect Physiol. 46 (7), 1111-1120 (2000)
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for
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Goto, S.G.
Direct Submission
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                                                                                                                                                                                                                                                                                  Calliphora vicina anterior fat body protein mRNA, complete cds. AY028616.1 GI:13488604
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BKWYYKAKIEGEDLAGFAVPYRGTTDGFAVGSGRRYVIVQMDGOVSETAKVLKTLFEVO
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ISNGLAWNEKTKKFYYIDTTDYEVKEYDYDFETGKASNPKVVFNLEKTSPKDHLLLDG
MTIDTGCNLYVATFNGHSIYKINPTTGQVLLEIKFPCKQITSAAFGGPNFHILFVTTS
SRFGEPHPAGTTXKYTGLGAKGYPWTKIQL"

223 C 231 G 358 L
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Hansen, I.A., Meyer, S.R., Schaefer, I. and Scheller, K.
Birect Submission
Submitted (17-MAR-2001) Cell and Developmental Biology, University
Wuerzburg, Biocenter Hubland, Wuerzburg D-97974, Germany
Location/Qualifiers
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                                                                                                                                      814
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in a yeast-2-hybrid interaction screen; CvAFP"
/codon_start=1
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                                                                   754
   694
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ATGGTCAAACAATTGATGAGGAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCGAA
                                                                                    689 ATGGCATGACCGTAGACACCGATGGCAATATCTACGTGGCCACCTTCAATGGTGGCACCG
                                                                 TTATTAAAATCAGTACCCAACAACCGGAAGTGTTACTGGATACCGTAAAATACCAGATC
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Calliphora vicina
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Osestroidea; Calliphoridae; Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interactor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hansen, I.A., Meyer, S.R., Schaefer, I. and Scheller, K.
Identification of the anterior fat body protein as inter
the hexamerin receptor in the blowfly Calliphora vicina
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/protein_id="AAK26174.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..1150
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/db_xref="taxon:7373"
/cell_type="trophocytes"
/tissue_type="anterior fat body"
/2..962
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Pred. No. 1.2e-13;
); Mismatches 358;
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ilarity 50.9%;
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Best Local Si
Matches 399,
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CDS

FEATURES

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/product="anterior fat body protein"
/product="anterior fat body protein"
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/protein_id="aAK51353.1"
/protein_id="arx13991405"
/translation="arx189405"
/translation="arx1894
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                                                                                                                                                                                                                                                                                                                                                                                             AF326959 1NV 08-MAY-2001 Calliphora vicina anterior fat body protein (AFP) mRNA, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 992)
Hansen, La., Meyer, S.R., Berlinger, M.J. and Scheller, K.
Identification of new interactors of the hexamerin receptor in the blowfly Calliphora vicina
                                                    785
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TTATTAAAATCAGTACCCAACAACGGAAGTGTTACTGGATACCGTAAAAATACCAGATC
                                      Gaps
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
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Submission

Direct Submission

Submission

Biocenter Hubland, Wuerzburg 97074, Germany

Location/Qualifiers

1. 992

/dev_stage="fat body"

/dev_stage="fat body"

/dev_stage="fat body"

/dev_stage="fat body"

/dev_stage="fat body"

/dev_stage="fat body"

/dev_stage="fat body"
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Pred. No. 4.2e-12;
0; Mismatches 310; Indels
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QNKVYKAKIEGEIFASFILPYBNKPQFEAVGGGLRTVIVQWDGVSAVAKVTRTLFEVQ
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DTDGNIYVAKFRFIDTNNHFYLAXDYNGSTGAYSNPKYIFDLKIRPEGPLFPDGMTV
DDDRAPATTGTGTVFKVNPSTGKILLEIKIPTTQITSVAFGGPNLDILYVTTANKF
260 c 249 g 226 t
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        Submitted (01-JUL-1999) Shin G Goto, Ohio State University, Department of Entomology; 1735 Neil Avenue, Columbus, OH 43210, USA (E-mail:shingoto@sci.osaka-cu.ac.jp, Tel:+1-614-292-4477, Fax:+1-614-292-2180)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 TIGGAGAAGGICCICACIGGGAICAIGAAACICAGACCIIAIAIITCGICGACACCGIAG 106
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                                                                                                                                                                                                                                                                                                                                                         /product="senescence marker protein-30 (SMP-30)"
/protein_id="BAA92938.1"
/db_xref="G1:7339662"
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                                                                                                                                                                        /organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 93.8; DB 3;
Pred. No. 8.3e-13;
0; Mismatches 382;
                                                                                                                                                                                              /strain-"Canton S"
/db_xref="taxon:7227"
/tissue_type="whole body"
/dev_stage="7 day adult stage"
                                                                                                                 Location/Qualifiers
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illarity 48.8%;
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AB036903 1155 bp mRNA linear INV 12-JUL-2000 Sarcophaga peregrina AFP mRNA for anterior fat body protein, complete cds.
AB036903 1 G1:8980620
AB036903.1 G1:8980620
AFP; anterior fat body protein.
Sarcophaga peregrina larva fat body cDNA to mRNA.
Sarcophaga peregrina larva fat body cBNA to mRNA.
Weoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Sarcophagae;
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Nakajima,Y and Natori,S.
Identification and characterization of an anterior fat body protein
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Pred. No. 5.8e-12;
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J. Biochem. 127 (5), 901-908 (2000)
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  /organism="Rattus sp."
/db_xref="taxon:10118"
a 231 c 309 g
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                221
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
CAATGATGGCAAGTGTGATCCTCGTGGTCGTTTGTTTGCCGGTACCATGCGTTATGTCGG
                                                                                                                                                                     339 TGAGGTAATCAAATCGGATGTGGGTATTTCCAATGGTTTGGCTTGGAATGAAGACAAAA
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                                                                                                                282 CGATGAATTCGAGCATCGTTA---TGGTGAATTATACAAGTACGAAAATGGAGGCGAAGT
                                                                                                                                                    447 AAAAATGCACGAGAGCAACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAA
                                                                                                                                                                                                                                                                  567 TACATTATCCATCAGCAATCAACGCCCATTATTTACTTTTGAAAAG-----CATGAAGT
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                                                                                              387 TGGTCTCCCCGTAGGACCGGTCACTGGCAGTTTATATCATTTAGGGGCTGATAAAAAGGT
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Yamaquchi, M.
Yamaquchi, M.
Patent: JP 1995123985-A 1 16-MAY-1995;
YAMAQUCHI MASAYOSHI, DAI ICHI PURE CHEM CO LTD
OR Rattus sp. (Rat)
PN JP 1995123985-A/1
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/organism='Rattus sp.'
80. .979
/product='Regucalcin'.
1. .1216
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C12N15/09,C12N1/21,(C12N1/21,C12R1:19);
strandedness: Double;
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E09237.1 GI:22025863
JP 1995123985-A/1.
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/translation="MSSIKIECVLRENYRCGESPVWEEASKCLLFVDIPSKTVCRWDS
ISNRVQRVGYDAPYSSVALRQSGYVATIGTKFCALNWEDOSYFILAMYDEDKKNNRF
NDGKVDDAGYRFAGTWAEFTARVLERHQGSLYSLFDDHSVKKYFNOYDISNGLDWSL
DHK IFYX IDSLSYYPOAFDYDLPTGOISNRRTVYKWENEDQIPDGMCIDVEGKLWVAC
NNGGRVIRLDPETGKRLQTVKLPVDKTTSCCFGGKDYSEMYVTCARDGMSAEGLLRQP
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      685
                                                                                                                                       TACCAGATCCTCAGGTCACCTCTGTAGCATTTGGCGGTCCGAATTTGGATGAACTGCATG 805
                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
     GATATCCAGATGGTCAAACAATTGATGAGGAGGGTAATTTATGGGTTGCCGTTTTCCAAG
                    GACAGCGAATTATTAAAATCAGTACCCAACAACCGGAAGTGTTACTGGATACCGTAAAAA
                                                                                                        GTTATACCATCTACAAAGTTAATCCCACTACCGGTAAAGTTTTGTTGGAAA---TTAAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleost
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Dec 8, 1994 this sequence version replaced gi:391851.
D16386:Submitted(07-Jun-1993)to DDBJ by:Masayoshi Yamaguchi.
Masayoshi Yamaguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ø
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                                                                                                                                                                                                                                                                                                                       ROD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                    rotein; regucalcin.
(strain:Wistar) liver cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (sites)
Shimokawa, N. and Yamaguchi, M.
Shimokawa, N. and Yamaguchi, M.
Molecular cloning and sequencing of the cDNA coding
calcium-binding protein regucalcin from rat liver
FEBS Lett. 327 (3), 251-255 (1993)
                                                                                                                                                                                                                                                                                                         Rat mRNA for calcium-binding protein, complete cds. D38467 D14327 D15386 D38467.1 G1:600378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.6%; Score 88.8; DB 10; 50.1%; Pred. No. 1.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.4e-11;
hes 293;
                                                                                                                                                                                                        806 TAACATCTGCTGGTCTTCAGCTTGACGACAGTTCT 840
                                                                                                                                                                                                                                       TCACAACATCTTCCCGTTTTGGTGAACCCGATCCT 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Graduate School of Nutritional Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="regucalcin"
/protein_id="BAA07490.1"
/db_xref="G1:408807"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAGNIFKITGLGVKGIAPYSYAG
1154. .1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 1594)
Shimokawa, N. and Yamaguchi, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 g
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                                                                                                                                                                                                                                                                                                                                                                                         calcium-binding protein;
Rattus norvegicus (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Shizuoka
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                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shizuoka 422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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BASE COUNT
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Best Local S
Matches 306
                                                                                                             186
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DEFINITION
ACCESSION
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REFERENCE
AUTHORS
JOURNAL
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TITLE
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RATCBP1
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               666 GCAAGGCTACAAATCCCAAGGTTGTTTTCAATCTACGCAAAAATAGTCCCAAGGATCATC 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               546 TAGTTAAATCTAACGTGGGTATTTCTAATGGTCTCGCTTGGAATGAAAAGACAAAAAAT 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --AGAAAACTITICATAAATATGTACCTTCTCAGAAA----AATACACGTTTTGTAAAG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 CTGGCAAACTCTTACGTTACAACTACAATGAAAATAAAGTGTACAAAGCAAAAATTGAAG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGAGGATTTAGCTGGTTTTGCTATACCTGTCGAAGGTACAACCGATCAGTTTGCCGTCG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GITIGGAACGIGAAATAGCCATICTTACAIGGGAIGGCGITAGIGCIGCACCTACAAGCA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281 'TAGAAGCTATTGTTAATGTCGAACC-----ACACATTAAAAATAACAGACTCAATG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 ATGGCAAAGCAGATCCCCTTGGCAATCTATGGACAGGTACAATGGCTATTGACGCTGGTC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  392 TCCCCGTAGGACCGGTCACTGGCAGTTTATATCATTTAGGGGCTGATAAAAAGGTAAAAA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGAATICGAACATCGITATGGTGAATTGTACAAATACGAAAAAGGTGGCAAAAITGAGG 545
                                               Lab.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 512 IGTATTATATTGATTCGGGGAAAAGAAGAGTAGACGAGTACGATTATGATGCTTCTACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  452 TGCACGAGAGCAACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  606 TCTATTACATTGATACCACTGACTATGAGGTCAAAGAATATGATTACGACTTTGAGACTG
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                                               Riken, Natori Special
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
                                             Submitted (06-JAN-2000) Yuki Nakajima, Riken, Natori Spe
Hirosawa2-1, Wako, Saltama 351-0198, Japan
(E-mail:nyuki@postman.riken.go.jp, Tel:+81-048-467-9439,
Fax:+81-048-462-4693)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 382;
                                                                                                                                             /organism="Sarcophaga peregrina"
/db_xref="taxon:7386"
/tissue_type="fat body"
/dev_stage="larva"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 89.8; DB 3;
Pred. No. 8.2e-12;
                                                                                                               Location/Qualifiers
2 (bases 1 to 1155)
Nakajima,Y. and Natori,S.
Direct Submission
Submitted (06-JAN-2000) Y
                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.7%;
                                                                                                                                                                                                                                /gene="AFP"
86. .1006
                                                                                                                                                                                                                                                                 /gene="AFP"
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406; Conservative
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Best Local 8
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/traislation="MSSIKIECVLRENYRCGESPVWEBASKCLLEVDIPSKTVCRWDS
ISNRYQRVGVDAPVSSVALRQSGGYVATIGTKFCALNWEDQSVFILAMVDEDKKNNRR
NDGKYDPAGTYRAETRAPALEHQGSIYSLFPDHSVKKYFDQVDISNGLDWSL
NDGKYDPAGTYRAETRAPULPTGOISNRRYKMEKDEOIPDGWCIDVEGKLWYAC
YNGGRYIRLDPETGKRLQTYKLPVDKTTSCCFGGKDYSEMYVTCARDGMSAEGLLRQP
DAGNIFKITGLGVKGIAPYSYAG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               664 GTTTACAAGATGGAAAAAGATGAA-----CAAATCCCAGATGGAATGTGCATTGATGTT 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCGAATTATTAAAATCAGTACCCAA 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 604 TACACTGTGGATGCCTTTGACTATGACCTGCCAACAGGACAGATTTCCAACCGCAGAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 CTATGGACAGGTACAATGGCTATTGACGCTGGTCTCCCCGTA---GGACCGGTCACTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                475 GCAAATGGCCTCGCCTGGAGTAATGATTTGAAGAAAATGTATTATTTGATTCGGGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1594;
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                                                                                                                   protein-30"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 85.6; DB 10;
Pred. No. 9e-11;
0; Mismatches 295;
                                                                                                                    /product="senescence marker
                                                                                                                                  /protein_id="CAA48786.1"
/db_xref="G1:57255"
/db_xref="SWISS-PROT:Q03336"
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                                                                                                                                                                                                                                                                                                                                                                                        464
     /db_xref="taxon:10116'
                    /dev_stage="6 months
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/gene="SMP30"
1566. .1571
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1588
                                               /gene="SMP30"
88. .987
                                                                                   /gene="SMP30"
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298 c
                                                                                                                                                                                                                                                                                                                                                                                                                                         tch 9.3%;
al Similarity 49.8%;
304; Conservative
                                    .1588
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955 AAAGGAATTGC 965
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Best Local S
Matches 304
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Sakaecho, Itabashi-ku,
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X69021 S48114
X69021.1 GI:57254
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Fujita,T., Shirasawa,T., Uchida,K. and Maruyama,N.
Isolation of CDNA clone encoding rat senescence marker (SMF30) and its tissue distribution
Biochim. Biophys. Acta 1132 (3), 297-305 (1992)
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35-2,
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/strain="Wistar/Sic"
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Submitted (08-DEC-1992) T. Fujita,
Metropolitan Inst. of Gerontology,
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/translation="MOSIKVECULRENYRCGESPVWEEASOSLLFVDIPSKIICRWDT
VSNOVQRVAVDAPVSSVALRQLGGYVATIGTRFCALNWENOSFVLAMVBEDKKNNRF
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DHKIFYXIDSLSYTVDAFDYDLQTGOISNRRLYKKMENDEQIPDGMCIDAEGKLWVAC
YNGGRVIRLDPETGKRLQTYKLPVDRTTSCCFGGKDYSEMYVTCARDGLNAEGLLROP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Submitted (24-JUN-1996) Masayoshi Yamaguchi, University of
Submitted (24-JUN-1996) Masayoshi Yamaguchi, University of
Shizuoka, Laboratory of Endocrinology and Molecular Metabolism,
Graduate School of Nurtritional Sciences; 52-1 Yada, Shizuoka,
Shizuoka 422, Japan (Tel:054-264-5580, Fax:054-264-580)
Sequence updated (15-Jul-1996) by: Masayoshi Yamaguchi.
Location/Qualifiers
                  715 CAACCGGAAGIGITACTGGAIACCGIAAAAAIACCAGAICCICAGGICACCICTGIAGCA
                                                                                                                                                  775 TITGGCGGTCCGAATTTGGATGAACTGCATGTAACATCTGCTGGTCTTCAGCTTGACGAC
GAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCGAATTATTAAAATCAGTACCCAA
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Murata,T. and Yamaguchi,M.
Molecular cloning of the cDNA coding for regucalcin and
expression in mouse liver: the expression is stimulated
administration
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Mus musculus mRNA for regucalcin, complete cds.
D86217
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Mus musculus liver CDNA to mRNA.
Mus musculus
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/db_xref="taxon:10090"
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/protein_id="BAA13046.1"
/db_xref="GI:1483152"
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207 c 282 g 31
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ISNRVQRVGAPVSSVALRQSGGYVATIGTKFCALNWEDGSVFILAMVDEDKKNNRF
NDGKVDPAGKFRGTRARETARAVLENHQSSLYSLFPDHSVKKYFDQVISNGLDWSL
DHKIFYYILDSLSYTVDAFDYDLPTGISNRFVYKMEKDEQTPDGMCIDVEGKLWVAC
YNGGRYIRLDPETGRRLQTVKLPVDKTTSCCFGGKDYSEMYYTCARDGMSAEGLLRQP
DAGNIFKITGLGVKGIAPYSYAG"
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Submitted (02-FEB-2000) Masayoshi Yamaguchi, Graduate School
Submitted (02-FEB-2000) Masayoshi Yamaguchi, Graduate School
Nutritional Sciences, University of Shizuoka, Laboratory of
Endocrinology and Molecular Metabolism; 52-1 Yada, Shizuoka
422-8526, Japan (E-mail:yamaguchéfnsl.u-shizuoka-ken.ac.jp,
Tel:+81-54-264-5580, Fax:+81-54-264-5580)
Location/Qualifiers
                                                                                                                                                        Raitus norvegicus hepatoma cell_line:H4-II-E cDNA to mRNA.
Rattus norvegicus
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                                                                   mRNA
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/organism="Rattus norvegicus"
/db_xref="ltaxon:10116"
/cell_line="H4-II-E"
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/protein_id="BAA90692.1"
/db_xref="G1:6970313"
                                                                   1605 bp
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99. .998
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Yamaguchi, M. and Misawa, H.
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                                                                                     norvegicus mRNA
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NDGRVDPAGRYFAGTMAEETAPAVLERHQGSLYSLFPDHSVKKYFDQVDISNGLDWSL
DHKIFYYIDSLSYTVDAFDYDLQTGOISNRRIYYKMEKDEQIPDGMCIDAEGKLWVAC
YNGGRVIRLDSLSYTVDAFDYDKTLPCCFGGKDYSEMYVTCARDGLNAEGLLRQP
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1132. .1137
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/db_xref="GI:1144000"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         409 TACTITGCTGGTACCATGGCTGAAACGGCCCCAGCTGTTCTTGAGCGCACCAAGGG 468
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                                                                                                               /product="senescence marker protein-30"
                                                                                                                                                                                                                                                                                                                                                             Score 80.8; DB 10;
Pred. No. 1.4e-09;
0; Mismatches 298;
   /tissue_type="liver"
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                   /dev_stage="adult"
1. .1573
                                                                                                                                                                                                                                                                                                                366
                                                                                                /codon_start=1
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1551. .1556
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/gene="SMP30"
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73. .972
                                                                              /gene="SMP30"
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ilarity 49.3%;
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Fujita, T., Shirasawa, T. and Maruyama, N.
Isolation and characterization of genomic and cbNA clones encoding mouse senescence marker protein-30 (SMP30)
Blochim. Blophys. Acta 1308 (1), 49-57 (1996)
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                                                                                           AGTITIATATCATTTAGGGGCTGATAAAAGGTAAAAATGCACGAGAGCAACATAGCTATA
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                                CTATGGACAGGTACAATGGCTATTGACGCTGGTCTCCCCGTA---GGACCGGTCACTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-JUN-1995) Takuji Shirasawa, Molecular Pathology, Tokyo Metropolitan Institute of Gerontology, 35-2, Sakaecho, Itabashi-ku, Tokyo 173, Japan Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 1573
/organism="Mus musculus"
/strain="C57Black/6"
/db_xref="taxon:10090"
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482 TCCTTGTACTCCCTCTTTCCTGATCACAGTGTGAAGAAATACTTTGACCAAGTGGATATC
                                                                                                                                                                                        602 TACACTGTGGATGCCTTTGACTATGACCTACAAACAGGACAGATTTCCAACCGCAGAATT
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                                                                                              542 ICCAATGGTTTGGATTGGTCCCTGGACCATAAAATCTTCTACTACATTGACAGCCTGTCC
                                                                                                                                             535 AGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTATCCATCAGCAATCAACGGCCA
                                                 475 GCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATATTGATTCGGGGAAA
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SVROVORVANDAPVSSYALLANGLGGYVATIGTKECALNWEDSOSYPVLANDDEDKKNNRF
NDGKVDDAGRYFGARFAEPARALERHQGSLYSLFPDHSVKKYFDQVDISNCLDWSL
DHKIFYYIDSLSYTVDAFDYDLQTQQISNRRIVYKMEKDEQIPDGMCIDABGKLWVAC
YNGGRYIRLDPETGKRLQTVKLPVDKTTSCCFGGKDXSEMYVTCARDGLNAEGLLRQP
DAGRYIRTGLGVKGIAPYTSCCFGGKDXSEMYVTCARDGLNAEGLLRQP
37 0 4 469 t
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                                BC012710 1598 bp mRNA linear ROD 07-AUG-2002 Mus musculus, Similar to regucalcin, clone MGC:14006 IMAGE:4210374,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCGAACCACACATTAAAATAACAGACTCAATGATGGCAAAGCAGATCCCCTTGGCAAT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 GIGGAIGAAGAIAAGAAAAATAATCGAITCAATGAIGGAAGGIGGAICCIGCIGGGAGA 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 18 Row: n Column: 22 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6677738. Location/Qualifiers
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1598)
                                                                                                                                                                                                                                                                                                                                                Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUM-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Email: gapbs.-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadandsystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="MGC:14006 IMAGE:4210374"
/tissue_type="Liver, normal. 5 month old male mouse."
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH108"
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Pred. No. 1.4e-09;
0; Mismatches 298; Indels 12;
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/protein_id="AAH12710.1"
/db_xref="G1:15215231"
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86, .985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/db_xref="taxon:10090"
/map="FVB/N"
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                                                                                                                                      BC012710.1 GI:15215230
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Best Local Similarity 49.33
Matches 301; Conservative
                                                                                       mRNA, complete cds
BC012710
                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                        Strausberg, R.
                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                     house mouse
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ORIGIN
                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
                                                                DEFINITION
                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                ACCESSION
                                                                                                                                      VERSION
KEYWORDS
SOURCE
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COMMENT
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